



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 103481

To: Laurie Scheiner
Location: CM1-8E12
Art Unit: 1648
Tuesday, September 16, 2003

Case Serial Number: 09/821877

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

103 481

From: Scheiner, Laurie
Sent: Tuesday, September 09, 2003 9:04 PM
To: STIC-Biotech/ChemLib
Subject: seq. search request

RECEIVED

SEP 10 2003

Please search SEQ ID NO:1 of application S.N. 09/821,877. Thanks!

STIC-BIOTECH DIVISION
(STIC)

Laurie Scheiner
Art Unit 1648
CM1 8E05
308-1122
8E12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 09-16-03

Searcher: Beverly C 4994

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

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Tue Sep 16 09:06:12 2003

US-09-821-877-1.rmpm

Scheiner, L.
09/18/21877 Page 1
Seq. ID 1 w/ Interf

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 01:28:16 ; Search time 2810 Seconds
(without alignments)
13938.229 Million cell updates/sec

Title: US-09-821-877-1

Perfect score: 1181
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues.

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						
1	1181	100.0	1181	1	PCT-US02-09227-1	Sequence 1, Appli
2	1181	100.0	1181	34	US-09-821-877-1	Sequence 1, Appli
3	1128.2	95.5	8007	35	US-09-837-297-3	Sequence 3, Appli
4	1117.2	94.6	1201	4	US-07-847-951A-218	Sequence 218, App

QY 1141 ATTTCTTTTGTCTTGGGTATATCAATTAAACCTTAATAA 1181
 DB 1141 ATTTCCTTTGCTTGGGTATATCAATTAAACCTTAATAA 1181

RESULT 2

US-09-821-877-1
 ; Sequence 1, Application US/09821877
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Coleman, Paul F.
 ; APPLICANT: Mushawar, Isa K.
 ; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
 ; TITLE OF INVENTION: And Methods Of Detection Thereof
 ; FILE REFERENCE: 6794.US.01
 ; CURRENT APPLICATION NUMBER: US/09/821,877
 ; NUMBER OF FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 1181
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B Virus
 ; US-09-821-877-1

Query Match 100.0%; Score 1181; DB 34; Length 1181;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAGAAATCTTTCACAGCAATCTCTGGAGATTCTTCCGACCAAGTTGAT 60
 DB 1 ATGGGGGAGAAATCTTTCACAGCAATCTCTGGAGATTCTTCCGACCAAGTTGAT 60
 QY 61 CGAGCTTCAGAGCAAAACCAACATCCAGATTGGAACTTAAATCCCAAGAACACC 120
 DB 61 CGAGCTTCAGAGCAAAACCAACATCCAGATTGGAACTTAAATCCCAAGAACACC 120
 QY 121 TGGCCAGAGCCCAACAGATAGAGCTGAGACATTGGAATGGGGTTACCCCAACGAC 180
 DB 121 TGGCCAGAGCCCAACAGATAGAGCTGAGACATTGGAATGGGGTTACCCCAACGAC 180
 QY 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAAGGATTAACAAACCTTGCAGCAAT 240
 DB 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAAGGATTAACAAACCTTGCAGCAAT 240
 QY 241 CGGCTCTCTGCTTCCACCAATGGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGG 300
 DB 241 CGGCTCTCTGCTTCCACCAATGGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 301 TTGAGAAACACTCATCTCAACGCATGAGTGAAGTCCCAAACTTTCACCAAACTCTG 360
 DB 301 TTGAGAAACACTCATCTCAACGCATGAGTGAAGTCCCAAACTTTCACCAAACTCTG 360
 QY 361 CAAGATCCAGAGTGAAGTGTGATATTTCCCTGCTGGGTCCAGTTTCAAGAAACAGTA 420
 DB 361 CAAGATCCAGAGTGAAGTGTGATATTTCCCTGCTGGGTCCAGTTTCAAGAAACAGTA 420
 QY 421 AACCTGTTCCGACTACTGTCTCTCCCATATGTCATATTTTCGAGAGATTGGGACCTT 480
 DB 421 AACCTGTTCCGACTACTGTCTCTCCCATATGTCATATTTTCGAGAGATTGGGACCTT 480
 QY 481 GCGCGGAACATGAGAAACATCATCAGATTCTAGGACCCCTGCTGTTTACAGGGG 540
 DB 481 GCGCGGAACATGAGAAACATCATCAGATTCTAGGACCCCTGCTGTTTACAGGGG 540
 QY 541 GGGTTTTTCTTGTGACAAAGATCTCTCAAAATCCGACAGATCTAGACTCGTGTGACT 600
 DB 541 GGGTTTTTCTTGTGACAAAGATCTCTCAAAATCCGACAGATCTAGACTCGTGTGACT 600
 QY 601 TCTCTCAATTTTCTAGGGGGAATCTACCGTGTCTTTGGCAAAATTCGAGTCCCAACC 660
 DB 601 TCTCTCAATTTTCTAGGGGGAATCTACCGTGTCTTTGGCAAAATTCGAGTCCCAACC 660

QY 661 TCCAACTACACCAACCTCTGCTCTTCCAACTTGTCTCTGATATGCTGATGCTG 720
 DB 661 TCCAACTACACCAACCTCTGCTCTTCCAACTTGTCTCTGATATGCTGATGCTG 720
 QY 721 CGGCTTTTATCATTTCTCTTTCATCTGCTGCTATGCTCATATTTCTTGTGTTCTT 780
 DB 721 CGGCTTTTATCATTTCTCTTTCATCTGCTGCTATGCTCATATTTCTTGTGTTCTT 780
 QY 781 CTGACATACAGAGTATGTTGCGGTGTCTCTTAAATCCAGATCTTCAACCAACGAC 840
 DB 781 CTGACATACAGAGTATGTTGCGGTGTCTCTTAAATCCAGATCTTCAACCAACGAC 840
 QY 841 ACGGACCATGACAGAGCTTGAACGACATCTCTGCTCAAGAACCTCATATCTCTCTGT 900
 DB 841 ACGGACCATGACAGAGCTTGAACGACATCTCTGCTCAAGAACCTCATATCTCTCTGT 900
 QY 901 TGCTGTACAAAACCTTGGAGTGAATCTGACCTGTATTTCCATCCATCTCTGGCT 960
 DB 901 TGCTGTACAAAACCTTGGAGTGAATCTGACCTGTATTTCCATCCATCTCTGGCT 960
 QY 961 TTGGAAATTCCTATGAGAGTGGGCTCAGGCGGTTCTCTGGCTGAGTTTACTAGT 1020
 DB 961 TTGGAAATTCCTATGAGAGTGGGCTCAGGCGGTTCTCTGGCTGAGTTTACTAGT 1020
 QY 1021 CCATTGTTCAAGTGTGATGAGGCTTTCCTCCCACTGTTTGGCTTCAATTATGATG 1080
 DB 1021 CCATTGTTCAAGTGTGATGAGGCTTTCCTCCCACTGTTTGGCTTCAATTATGATG 1080
 QY 1081 ATGTTGACTGGGGGCCAAGTCTGACACCATCTTGAATCTCTTTTACCGCTGTACCA 1140
 DB 1081 ATGTTGACTGGGGGCCAAGTCTGACACCATCTTGAATCTCTTTTACCGCTGTACCA 1140
 QY 1141 ATTTCTTTTGTCTTGGGTATATCAATTAAACCTTAATAA 1181
 DB 1141 ATTTCTTTTGTCTTGGGTATATCAATTAAACCTTAATAA 1181

RESULT 3

US-09-837-297-3
 ; Sequence 3, Application US/09837297
 ; GENERAL INFORMATION:
 ; APPLICANT: RYU, WANG SHICK
 ; TITLE OF INVENTION: Hepatitis B virus vectors for gene therapy
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/837,297
 ; PRIOR APPLICATION NUMBER: KR2000-21070
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Koparentin 1.71
 ; SEQ ID NO: 3
 ; LENGTH: 8007
 ; TYPE: DNA
 ; ORGANISM: HBV
 ; FEATURE:
 ; NAME/KEY: gene
 ; LOCATION: (1)..(8007)
 ; OTHER INFORMATION: Prototype vector of HBV
 ; US-09-837-297-3

Query Match 95.5%; Score 1128.2; DB 35; Length 8007;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1148; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGGGGAGAAATCTTTCACAGCAATCTCTGGAGATTCTTCCGACCAAGTTGAT 60
 DB 1021 ATGGGGGAGAAATCTTTCACAGCAATCTCTGGAGATTCTTCCGACCAAGTTGAT 1090
 QY 61 CGAGCTTCAGAGCAAAACCAACATCCAGATTGGAACTTAAATCCCAAGAACACC 120
 DB 1091 CGAGCTTCAGAGCAAAACCAACATCCAGATTGGAACTTAAATCCCAAGAACACC 1150
 QY 121 TGGCCAGAGCCCAACAGATAGAGCTGAGACATTGGAATGGGGTTACCCCAACGAC 180

Db 1151 TGCCAGACGCCAACAAAGTAGAGCTGGAGCAATGGGGCTGGGGTTTCAACCCACGCGAC 1210
QY 181 GAGGCGCTTTTGGGGTGGAGACCTCTAGGCTCAGGGGCTAACACAAACCTTGGCCAGCAAT 240
Db 1211 GAGGGCGCTTTTGGGGTGGAGACCTCTAGGCTCAGGGGCTACTACAAATTTTGGCCAGCAAT 1270
QY 241 CGGCTCTCTGCTTCCACCAATCGCAGTCAAGAAAGCAGCTACCCGCTGTCTCCACT 300
Db 1271 CGGCTCTCTGCTTCCACCAATCGCAGTCAAGAAAGCAGCTACCCGCTGTCTCCACT 1330
QY 301 TTGAGAAACATCATCTCTCAAGCCATGAGTGAATCTCAACATTTTCCACCAACTCTG 360
Db 1331 TTGAGAAACATCATCTCTCAAGCCATGAGTGAATTTCCAAACCTTCCACCAACTCTG 1390
QY 361 CAAGATCCGAGTGAAGGCTGTATTTCCGCTGGTGGCTCCAGTTTGAAGAAAGTA 420
Db 1391 CAAGATCCGAGTGAAGGCTGTATTTCCGCTGGTGGCTCCAGTTTGAAGAAAGTA 1450
QY 421 AACCTGTCTGACTACTGTCTCTCCATATCGTCAATCTTCTCGAGAGTTGGGAGCCCT 480
Db 1451 AACCTGTCTGACTACTGTCTCTCCATATCGTCAATCTTCTCGAGAGTTGGGAGCCCT 1510
QY 481 GCGCGAAACATGAGAAACATCATCATGAGATTCTTGAAGACCTCTGCTGTATCAGGCG 540
Db 1511 GCGCTGAACATGAGAAACATCATCATGAGATTCTTGAAGACCTCTGCTGTATCAGGCG 1570
QY 541 GGGTTTTTCTGTGTGCAAGAAATCTTCAAAATCCGAGAGTCTAGACTGTGGTGGACT 600
Db 1571 GGGTTTTTCTGTGTGCAAGAAATCTTCAAAATCCGAGAGTCTAGACTGTGGTGGACT 1630
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Db 1631 TCTCTCAATTTTCTAGGGGAACTACCGTGTGTCTTGGCCAAAATTTGCGAGTCCCAACC 1690
QY 661 TCCAAATCTACCAACCTCTCTGTCTTCCAACTTGTCTGGTTATTCGCTGAGTGTCTG 720
Db 1691 TCCAAATCTACCAACCTCTCTGTCTTCCAACTTGTCTGGTTATTCGCTGAGTGTCTG 1750
QY 721 CGGCGTTTTTCAATCTCTCTCTTCAATCTGCTGATAGCCCTCAATCTTGTGGTCTT 780
Db 1751 CGGCGTTTTTCAATCTCTCTCTTCAATCTGCTGATAGCCCTCAATCTTGTGGTCTT 1810
QY 781 CTGGAATCATGAGTATGTGGCCGTTGTCTCTTAATTCAGAGATTTCAACACGACG 840
Db 1811 CTGGAATCATGAGTATGTGGCCGTTGTCTCTTAATTCAGAGATTTCAACACGACG 1870
QY 841 ACGGAGCATGACAGGCTTGACGCTCTGCTCAAGAAACCTTATGTAATCCCTCTGT 900
Db 1871 ACGGAGCATGACGAGCTTGACGCTCTGCTCAAGAAACCTTATGTAATCCCTCTGT 1930
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Db 1991 TTGCGAAATTTCTATGGAGTGGGCTCAGCCGTTTCTCTGCTCAAGTTTACTAGT 2050
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Db 2051 CCATTTTCAAGTGTGTAAGGCTTTCCGCCACTGTTTGGCTTCAAGTTATATGATG 2110
QY 1081 ATGTGTACTGGGGGCAAGCTGTATACCACTTGTAGTCCCTTTTACCGGCTTTACA 1140
Db 2111 ATGTGTACTGGGGGCAAGCTGTATACCACTTGTAGTCCCTTTTACCGGCTTTACA 2170
QY 1141 ATTTCTTTTGTCTTGGGTATACATTTAAACCTTAATAA 1181
Db 2171 ATTTCTTTTGTCTTGGGTATACATTTAAACCTTAATAA 2211

RESULT 4

US-07-847-951A-218
; Sequence 218, Application US/07847951A
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/847,951A
; FILING DATE: 19920326
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-847-951A-218

Query Match 94.6%; Score 1117.2; DB 4; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGGCGAGAAATTTTCCACAGCAATCTCTGGGATTTCTTCCGACGACGAGTTGAT 60
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Db 92 CAGGCTTCAAGCAAAACCAACCAATTCAGATTGGACTTCAATCCCAAGACACC 151
QY 121 TGCGCAGAGCCCAACAAAGTAGAGGCTGGAGCAATGGGAGTTGAGTCCACCCGCGAC 180
Db 152 TGCGCAGAGCCCAACAAAGTAGAGGCTGGAGCAATGGGAGTTGAGTCCACCCGCGAC 211
QY 181 GAGGCGCTTTTGGGGTGGAGGCTCAGGCTCAGGGGATTAACAAACCTTGGCCAGCAAT 240
Db 212 GAGGCGCTTTTGGGGTGGAGGCTCAGGCTCAGGGGATTAACAAACCTTGGCCAGCAAT 271
QY 241 CGGCTCTCTGCTTCCACCAATGCGCAGTCAAGAAAGCAGCTTACCCGCTGTCTCCACT 300
Db 272 CGGCTCTCTGCTTCCACCAATGCGCAGTCAAGAAAGCAGCTTACCCGCTGTCTCCACT 331
QY 301 TTGAGAAACATCATCTCTCAAGCCATGAGTGAATCTCAACATTTTCCACCAACTCTG 360
Db 332 TTGAGAAACATCATCTCTCAAGCCATGAGTGAATTTCCAAACCTTTTCCAAACTCTG 391
QY 361 CAAGATCCGAGTGAAGGCTGTATTTCCGCTGGTGGCTCCAGTTTGAAGAAAGTA 420
Db 392 CAAGATCCGAGTGAAGGCTGTATTTCCGCTGGTGGCTCCAGTTTGAAGAAAGTA 451
QY 421 AACCTGTCTGACTACTGTCTCTCCATATCGTCAATCTTCTCGAGAGTTGGGAGCCCT 480

Db 452 AACCTGTCGACTGCTCTCCCTTATCTGCAATCTTCTCGAGATGGGAGACCT 511
 Qy 481 GCGGGAACATGAGAACATCATCAGAGATTCCTAGAGACCCCTGCTCGTTTACAGGCG 540
 Db 512 GCGCTGAAATGAGAAATCATCATGAGATTCCTAGAGACCCCTGCTCGTTTACAGGCG 571
 Qy 541 GGGTTTCTTGTGACAGAAATCTCACAATACCGAGAGTCTAGACTCGTGTGAGACT 600
 Db 572 GGGTCTTCTGTGACAGAAATCTCACAATACCGAGAGTCTAGACTCGTGTGAGACT 631
 Qy 601 TCTCTCAATTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 660
 Db 632 TCTCTCAATTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 691
 Qy 661 TCCATCATCTACCAACCTCTGCTCTCAACTGCTCGTATGCTGAGAGTGTCTG 720
 Db 692 TCCATCATCTACCAACCTCTGCTCTCAACTGCTCGTATGCTGAGAGTGTCTG 751
 Qy 721 CGGCGTTTATCATCTTCTCTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 752 CGGCGTTTATCATCTTCTCTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
 Qy 781 CTGAGCTATCAAGATGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 812 CTGAGCTATCAAGATGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
 Qy 841 AGGGAGCATGAGAGCTGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 872 AGGGAGCATGAGAGCTGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
 Qy 901 TCTCTGACAAACCTTCGAGTGAAGAACTGCACTGATTCCTGCTGCTGCTGCTGCT 960
 Db 932 TCTCTGACAAACCTTCGAGTGAAGAACTGCACTGATTCCTGCTGCTGCTGCTGCT 991
 Qy 961 TTGCGAAATTCCTATGAGAGTGGGCTGAGCCGCTTCTGCTGCTGCTGCTGCTGCT 1020
 Db 992 TTGCGAAATTCCTATGAGAGTGGGCTGAGCCGCTTCTGCTGCTGCTGCTGCTGCT 1051
 Qy 1021 CCATTTGTCAGTGGTCTGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 Db 1052 CCATTTGTCAGTGGTCTGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
 Qy 1081 ATGTTGTAAGGGGCAAGTCTGTAACACCTTGTAGTCCCTTTTACCGCTGTTACCA 1140
 Db 1112 ATGTTGTAAGGGGCAAGTCTGTAACACCTTGTAGTCCCTTTTACCGCTGTTACCA 1171
 Qy 1141 ATTTCTTTTGTCTTGGGTATACATTTAA 1170
 Db 1172 ATTTCTTTTGTCTTGGGTATACATTTAA 1201

RESULT 5
 US-08-036-218-216
 Sequence 216, Application US/08036218
 GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo
 APPLICANT: Perkus, Marion E.
 APPLICANT: Taylor, Jill
 APPLICANT: Tartaglia, James
 APPLICANT: Norton, Elizabeth K.
 APPLICANT: Riviere, Michel
 APPLICANT: de Taisne, Charles
 APPLICANT: Limbach, Keith J.
 APPLICANT: Johnson, Gerard P.
 APPLICANT: Pincus, Steven E.
 APPLICANT: Cox, William I.
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE STRAIN
 NUMBER OF SEQUENCES: 221
 CORRESPONDENCE ADDRESS:
 ADDRESSES: William S. Frommer c/o
 ADDRESSES: Curtis, Morris & Safford, P.C.
 STREET: 530 Fifth Avenue
 CITY: New York

STATE: New York
 COUNTRY: United State of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/036,218
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/713,967
 FILING DATE: 11-JUN-1991
 APPLICATION NUMBER: US 07/666,056
 FILING DATE: 07-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 216:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1201 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-036-218-216

Query Match 94.6%; Score 1117.2; DB 5; Length 1201;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 ATGGGAGCAATCTTCCACAGCAATCTCTGGAGTCTTCCGACACAGTTGAT 60
 Db 32 ATGGGAGCAATCTTCCACAGCAATCTCTGGAGTCTTCCGACACAGTTGAT 91
 Qy 61 CCAGCTTCAGAGCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACAC 120
 Db 92 CCAGCTTCAGAGCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACAC 151
 Qy 121 TGGCCAGAGCCCAACAGATGAGAGCTGAGATTCGAGATCGAGGCTTACCCACCGAC 180
 Db 152 TGGCCAGAGCCCAACAGATGAGAGCTGAGATTCGAGGCTTACCCACCGAC 211
 Qy 181 GGAGGCTTTGGGGTGGAGCCCTCAGGCTCAGGCAATTAACCAACCTTGCAGCAAT 240
 Db 212 GGAGGCTTTGGGGTGGAGCCCTCAGGCTCAGGCAATTAACCAACCTTGCAGCAAT 271
 Qy 241 CGGCTCTGCTTCCACCAATGCGAGTCCAGAGAGGAGCCGCTGCTCCACT 300
 Db 272 CGGCTCTGCTTCCACCAATGCGAGTCCAGAGAGGAGCCGCTGCTCCACT 331
 Qy 301 TTGAGAAACATCTATCTTCAGGCTGAGGATTCGCAAACTTTCCACCAACTCTG 360
 Db 332 TTGAGAAACATCTATCTTCAGGCTGAGGATTCGCAAACTTTCCACCAACTCTG 391
 Qy 361 CAAGATCCAGAGTGAAGGCTGATTTCCCTGCTGAGGCTGAGGATTCAGGAGAGTA 420
 Db 392 CAAGATCCAGAGTGAAGGCTGATTTCCCTGCTGAGGCTGAGGATTCAGGAGAGTA 451
 Qy 421 AACCTGTTCCGACTGCTCTCTCCATTCGATTCATCTTCTCGAGATTGGGAGCCT 480
 Db 452 AACCTGTTCCGACTGCTCTCTCCATTCGATTCATCTTCTCGAGATTGGGAGCCT 511
 Qy 481 GCGGGAACATGAGAACATCATCAGAGATTCCTAGAGACCCCTGCTCGTTTACAGGCG 540
 Db 512 GCGGGAACATGAGAACATCATCAGAGATTCCTAGAGACCCCTGCTCGTTTACAGGCG 571
 Qy 541 GGGTTTCTTGTGACAGAAATCTCACAATACCGAGAGTCTAGACTCGTGTGAGACT 600

081036,217

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|||||
Db 572 GGGTCTCTTGTGACAAATCTCACAATACCGAGAGTCTAGACTCGTGGTACT 631
Qy 601 TCTCTCAATTTTCTAGGGGGAACACCGAGTGTCTGGGCAAAATTCGAGTCCCAAC 660
Db 632 TCTCTCAATTTTCTAGGGGGAACACCGAGTGTCTGGGCAAAATTCGAGTCCCAAC 691
Qy 661 TCCAACTCACTCAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 692 TCCAACTCACTCAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 751
Qy 721 CGGCGTTTATCATCT 780
Db 752 CGGCGTTTATCATCT 811
Qy 781 CTGAGCATCAAGATAGTGTGCGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 812 CTGAGCATCAAGATAGTGTGCGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 871
Qy 841 ACGGACATGACAGAGCTGACAGACTCTGCTCAAGAACTCTATGTATCCCTCTCT 900
Db 872 ACGGACATGACAGAGCTGACAGACTCTGCTCAAGAACTCTATGTATCCCTCTCT 931
Qy 901 TCGCTGACAAACCTTCTGATGAACTGCACTGTATCTCCATCCCATCATCTCTGCT 960
Db 932 TCGCTGACAAACCTTCTGATGAACTGCACTGTATCTCCATCCCATCATCTCTGCT 991
Qy 961 TTGGGAAATTTCTATGAGAGTGGGAGCTGAGCCGTTCTCCGGCTCACTTATAGT 1020
Db 992 TTGGGAAATTTCTATGAGAGTGGGAGCTGAGCCGTTCTCCGGCTCACTTATAGT 1051
Qy 1021 CCATTTGTTGATGTTCTGATGAGGCTTTCCTCCCACTGTTTGCTTCAAGTATAGAT 1080
Db 1052 CCATTTGTTGATGTTCTGATGAGGCTTTCCTCCCACTGTTTGCTTCAAGTATAGAT 1111
Qy 1081 ATGTTGATCTGGGGGGAAGTCTGTACACATCTTGAAGTCCCTTTTACCGCTGTTA 1140
Db 1112 ATGTTGATCTGGGGGGAAGTCTGTACACATCTTGAAGTCCCTTTTACCGCTGTTA 1171
Qy 1141 ATTTCTTTGTTGTTGGGTATACATTTAA 1170
Db 1172 ATTTCTTTGTTGTTGGGTATACATTTAA 1201

RESULT 6
US-07-847-951A-215
Sequence 215, Application US/07847951A
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Saford
ADDRESS: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,951A
FILING DATE: 19920326
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEO ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-847-951A-215

Query Match 94.6%; Score 1117.2; DB 4; Length 1285;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGGGGCAGAAATCTTCCACAGCATCCCTCGGGATCTCTCCGACACAGGTTGGAT 60
Db 116 ATGGGGCAGAAATCTTCCACAGCATCCCTCGGGATCTCTCCGACACAGGTTGGAT 175
Qy 61 CCAGCTTTCAGAGCAACACCAACAAATTCAGATTGGGACTTCAATCCCAAGAGACACC 120
Db 176 CCAGCTTTCAGAGCAACACCAACAAATTCAGATTGGGACTTCAATCCCAAGAGACACC 235
Qy 121 TGGCCAGAGCCCAAGAGTGGAGCTGAGACATTTGGAGTGGGGTTACCCCAACGAC 180
Db 236 TGGCCAGAGCCCAAGAGTGGAGCTGAGACATTTGGAGTGGGGTTACCCCAACGAC 295
Qy 181 GAGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACAACTTGGCAGCAAT 240
Db 296 GAGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACAACTTGGCAGCAAT 355
Qy 241 CGGCTCTCTGCTTTCACCAATCCAGTCAAGAGGCAAGGCAAGCTACCCGCTGTCCACCT 300
Db 356 CGGCTCTCTGCTTTCACCAATCCAGTCAAGAGGCAAGGCAAGCTACCCGCTGTCCACCT 415
Qy 301 TTGAGAAACATATCTCTCAAGCATGACAGTGGAACTCCACAACTTTCACCAACTCTG 360
Db 416 TTGAGAAACATATCTCTCAAGCATGACAGTGGAACTCCACAACTTTCACCAACTCTG 475
Qy 361 CAGATCCCGAGTGAAGGCTGTATTTCCCTGGTGGGCTCCAGTTCCAGGACAGTA 420
Db 476 CAGATCCCGAGTGAAGGCTGTATTTCCCTGGTGGGCTCCAGTTCCAGGACAGTA 535
Qy 421 AACCTGTTCCGACTGCTCTCTCCATATCTCATATCTTCTCGAGATTTGGGAGCCCT 480
Db 536 AACCTGTTCCGACTGCTCTCTCCATATCTCATATCTTCTCGAGATTTGGGAGCCCT 595
Qy 481 GCGGGAACTGGAGAAACATCAGATGAGATTCTTGAAGCCCTGCTCTGTGTTACAGGCG 540
Db 596 GCGCTGAACATGAGAAACATCAGATGAGATTCTTGAAGCCCTGCTCTGTGTTACAGGCG 655
Qy 541 GGGTTTTTCTGTTGAAGAATCTCAAAATCCGACAGTCTAGACTGGTGGTACT 600
Db 656 GGGTTTTTCTGTTGAAGAATCTCAAAATCCGACAGTCTAGACTGGTGGTACT 715
Qy 601 TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 660
Db 716 TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 775
Qy 661 TCCAACTCACTCAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 776 TCCAACTCACTCAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 835
Qy 721 CGGCGTTTATCATCT 780
Db 836 CGGCGTTTATCATCT 895
Qy 781 CTGAGCATCAAGATAGTGTGCGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 896 CTGAGCATCAAGATAGTGTGCGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 955
Qy 841 ACGGACATGACAGAGCTGACAGACTCTGCTCAAGAACTCTATGTATCCCTCTCTGT 900

Db 956 ACGGACCATGCCGACCTGATGACTGCTCAAGAACTTATGATCCCTCTGT 1015
QY 901 TCGTGTACAAAACCTTCGGATGGAAGTACCTGATCCATCCATCCTGGGCT 960
Db 1016 TCGTGTACAAAACCTTCGGATGGAAGTACCTGATCCATCCATCCTGGGCT 1075
QY 961 TTGGGAAAATTCCTATGAGAGTGGGCTTCAGCCGTTTCTCTGGCTCAAGTTACTAGTG 1020
Db 1076 TTGGGAAAATTCCTATGAGAGTGGGCTTCAGCCGTTTCTCTGGCTCAAGTTACTAGTG 1135
QY 1021 CCATTTGTTCAGTGTGTCTAGGAGCTTTCCTCCCACTGTTGGCTTCAAGTTATGAGATG 1080
Db 1136 CCATTTGTTCAGTGTGTCTAGGAGCTTTCCTCCCACTGTTGGCTTCAAGTTATGAGATG 1195
QY 1081 ATGTGTACTGGGGGCAAGCTGTATACACATCTTGAGTCCCTTTTACCGCTGTACCA 1140
Db 1196 ATGTGTACTGGGGGCAAGCTGTATACACATCTTGAGTCCCTTTTACCGCTGTACCA 1255
QY 1141 ATTTTCTTTTGTCTTTGGTATACATTTAA 1170
Db 1256 ATTTTCTTTTGTCTTTGGTATACATTTAA 1285

RESULT 7

US-08-036-218-213

Sequence 213, Application US/08036218

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: Norton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE STRAIN
NUMBER OF SEQUENCES: 221

CORRESPONDENCE ADDRESS:

ADDRESSEE: William S. Frommer C/O
ADDRESSER: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United State of America
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,218

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/713,967
FILING DATE: 11-JUN-1991
APPLICATION NUMBER: US 07/666,056
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 213:

SEQUENCE CHARACTERISTICS:

LENGTH: 1285 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-08-036-218-213

Query Match 94.6%; Score 1117.2; DB 5; Length 1285;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGGGCAAGAACTCTTCACCAAGCAATCTCTGGGATCTTTCCGACACCAAGTTGAT 60
Db 116 ATGGGGCAAGAACTCTTCACCAAGCAATCTCTGGGATCTTTCCGACACCAAGTTGAT 175
QY 61 CCAGCTTCAGAGCAAAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACACC 120
Db 176 CCAGCTTCAGAGCAAAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACACC 235
QY 121 TGGCCAGAGCCCAAGAGTGAAGCTGGAAGATTGGAGCTGGGGTTCACCCAAGCAGC 180
Db 236 TGGCCAGAGCCCAAGAGTGAAGCTGGAAGATTGGAGCTGGGGTTCACCCAAGCAGC 295
QY 181 GGAGGCTTTGGGGTGGAGCCCTCAGGCTCAGGCGATTAACAACCTTGGCAGCAAT 240
Db 296 GGAGGCTTTGGGGTGGAGCCCTCAGGCTCAGGCGATTAACAACCTTGGCAGCAAT 355
QY 241 CGGCTCTGCTGCTTCACCAATGCGCAGTCAAGAAAGGACCTACCCGCTGTCTCACT 300
Db 356 CGGCTCTGCTGCTTCACCAATGCGCAGTCAAGAAAGGACCTACCCGCTGTCTCACT 415
QY 301 TTGAGAAACACTCATCTCTCAAGCCATGCAATGCAATCTCAACACTTTCCACCAACTCTG 360
Db 416 TTGAGAAACACTCATCTCTCAAGCCATGCAATGCAATCTCAACACTTTCCACCAACTCTG 475
QY 361 CAAGATCCCAAGAGAGAGGCTGTATTTCCCTGCTGGTGGCTCAGTTCCAGGACAGTA 420
Db 476 CAAGATCCCAAGAGAGAGGCTGTATTTCCCTGCTGGTGGCTCAGTTCCAGGACAGTA 535
QY 421 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTCTCGAGATTGGGAGCCT 480
Db 536 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTCTCGAGATTGGGAGCCT 595
QY 481 GCGCGAAACATGAGAACATCAATCAGGATTCCTAGGACCCCTGCTGTCTTACAGGCG 540
Db 596 GCGCGAAACATGAGAACATCAATCAGGATTCCTAGGACCCCTGCTGTCTTACAGGCG 655
QY 541 GGGTTTCTTCTGTGACAAGAACTCTCAATATCCGAGAGCTTGAATCGTGATGCT 600
Db 656 GGGTTTCTTCTGTGACAAGAACTCTCAATATCCGAGAGCTTGAATCGTGATGCT 715
QY 601 TCTCTCAATTTCTAGGGGGAACCTACGCTGTGTCTTGGCCAAATTCGACGCCCCAAC 660
Db 716 TCTCTCAATTTCTAGGGGGAACCTACGCTGTGTCTTGGCCAAATTCGACGCCCCAAC 775
QY 661 TCCATCACTACCAACCTCTGTCCTCAACTTGTCTGTTATCGCTGATGATGCTG 720
Db 776 TCCATCACTACCAACCTCTGTCCTCAACTTGTCTGTTATCGCTGATGATGCTG 835
QY 721 CGGCTTTTATCATCTTCTCTTCAATCTGCTGTATGCTTCAATCTTCTTGTGATCTT 780
Db 836 CGGCTTTTATCATCTTCTCTTCAATCTGCTGTATGCTTCAATCTTCTTGTGATCTT 895
QY 781 CTGACATCAAGGATGTGGCCGCTGTGTCTTCAATTCAGAGATCTTCAACGACGAC 840
Db 896 CTGACATCAAGGATGTGGCCGCTGTGTCTTCAATTCAGAGATCTTCAACGACGAC 955
QY 841 ACGGACCATGACAGCTGACAGACTCTGCTCAAGAACCTTATGATTCCTCTGT 900
Db 956 ACGGACCATGACAGCTGACAGACTCTGCTCAAGAACCTTATGATTCCTCTGT 1015
QY 901 TCGTGTACAAAACCTTCGGATGGAAGTACCTGATTCCTCCATCCATCCTGGGCT 960
Db 1016 TCGTGTACAAAACCTTCGGATGGAAGTACCTGATTCCTCCATCCATCCTGGGCT 1075
QY 961 TTGGGAAAATTCCTATGAGAGTGGGCTTCAGCCGTTTCTCTGGCTCAAGTTACTAGTG 1020

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Db 1076 TTGGGAAATTCCTATGGAGTGGGCTTCAGCCGTTTCTCGGCTCAGTTTACTAGTG 1135
Qy 1021 CCATTGTTAGAGTGTCGAGGGCTTTCCGCCAGCTTTGGCTTCAAGTATATGATG 1080
Db 1136 CCATTGTTAGAGTGTCGAGGGCTTTCCGCCAGCTTTGGCTTCAAGTATATGATG 1195
Qy 1081 ATGTTGACTGGGGGCCAAGCTGTATACCACTTTGAGTCCCTTTTACCGCTGTACCA 1140
Db 1196 ATGTTGATTTGGGGGCCAAGCTGTATACCACTTTGAGTCCCTTTTACCGCTGTACCA 1255
Qy 1141 ATTTCTTTTGTCTTTGGGTATACATTAA 1170
Db 1256 ATTTCTTTTGTCTTTGGGTATACATTAA 1285

RESULT 8
US-10-130-915-1
; Sequence 1, Application US/10130915
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; APPLICANT: Schinazi, Raymond
; APPLICANT: De Gendt, Sija
; APPLICANT: Van Geyt, Carolina
; APPLICANT: Zoulim, Fabien
; APPLICANT: Fried, Michael
; APPLICANT: Rosseau, Rudi
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR A NEW
; TITLE OF INVENTION: GENOTYPE OF HEPATITIS B VIRUS
; FILE REFERENCE: 16117.000102
; CURRENT APPLICATION NUMBER: US/10/130.915
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/US00/32108
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/167,206
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Note:
; OTHER INFORMATION: Artificial Sequence = synthetic construct
US-10-130-915-1

Query Match 86.4%; Score 1020.6; DB 46; Length 3248;
Best Local Similarity 91.6%; Pred. No. 4.8e-289;
Matches 1080; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 3 GGGGCAATCTTTCCAGCAGCATCTCTGGGATTTCTTCCGACGACGAGTTGATCC 62
Db 1103 GGGAAAGACCTTTCCGCGCAGCATCTCTAGAGATCTTCCGATACCAAGTTGGACCC 1162
Qy 63 AGCCTTCAGAGCAAAACCAACATCCAGATTGGAGCTTCATCCCAAGAGACCTG 122
Db 1163 AGCATTCAGAGCAAAATCCAAATCCAGATTGGAGCTTCATCCCAAAAGACCTTG 1222
Qy 123 GCCAGAGCCCAACAGTAGAGCTGAGCATTTGGAGCTGGGGTTTACCCGACGG 182
Db 1223 GCCAGAGCCCAACAGTAGAGCTGAGCATTTGGAGCTGGGGTTTACCCGACGG 1282
Qy 183 AGGCTTTTGGGGGAGGAGCCCTCAGGCTCAGGGGATTAACAACAACCTTTGACGAATCC 242
Db 1283 AGGCTTTTGGGGGAGGAGCCCTCAGGCTCAGGGGATTAACAACAACCTTTGACGAATCC 1342
Qy 243 GCCTCTGCTTCCACCAATCCGAGTGAAGAGGACGCTTACCCGCTGTCTCCACTTT 302
Db 1343 GCCTCTGCTTCCACCAATCCGAGTGAAGAGGACGCTTACCCGCTGTCTCCACTTT 1402
Qy 303 GAGAAACACTGATCTTCAAGCATGAGTGAATCTCAACAATTTCACCAACTCTGCA 362
Db 1403 GAGAAACACTGATCTTCAAGCATGAGTGAATCTTCAACAATTTCACCAACTCTTACA 1462
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Qy 363 AGATCCCAAGTAGAGAGTCTGATTTCCCTGCTGAGCTCCAGTTCAAGAACTAA 422
Db 1463 AAATCCCAAGTAGAGAGCTGATTTCCCTGCTGAGCTCCAGTTCAAGAACTAA 1522
Qy 423 CCTGTTCCGACTAGTCTCTCCCAATATGCTCAATCTTTGTGAGATTGGGACCTTCG 482
Db 1523 CCTGTTCCGACTAGTCTCTCCCAATATGCTCAATCTTTGTGAGATTGGGACCTTCG 1582
Qy 483 GGGGAACATGAGAAATACATCAATCAGATTTCAGAGACCCGCTGTTTACAGCGGG 542
Db 1583 ACCGAACATGAGAAATACATCAATCAGATTTCAGAGACCCGCTGTTTACAGCGGG 1642
Qy 543 GTTTTCTTGTGACAAAGATCTCTCAAAATCCGAGAGCTTACCTGCTGTGAGACTTC 602
Db 1643 GTTTTCTTGTGACAAAGATCTCTCAAAATCCGAGAGCTTACCTGCTGTGAGACTTC 1702
Qy 603 TCTCAATTTTCTAGGGGAACTACCGCTGTCTTGGCCAAATTCGAGTCCCAACTTC 662
Db 1703 TCTCAATTTTCTAGGGGAGTGCCTGTCTCTGAGCTTAAATTCGAGTCCCAACTTC 1762
Qy 663 CAATCACTACCAACCTCTCTCTCTCCCACTGTCCTGATATGCTGATATGCTGGG 722
Db 1763 CAATCACTACCAACCTCTCTCTCTCCCACTGTCCTGATATGCTGATATGCTGGG 1822
Qy 723 GCCTTTATCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 1823 GCCTTTATCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1882
Qy 783 GGAATATCAAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
Db 1883 GGAATATCAAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1942
Qy 843 GGGACCATGAGAGCCTGACGACCTCTGCTCAAGAACCTATGATCCCTGCTG 902
Db 1943 GGGACCATGAGAGCCTGACGACCTCTGCTCAAGAACCTATGATCCCTGCTG 2002
Qy 903 GTGTACAAACCTTCCGATGGAACCTGATATTTCCATCCATCATCTCTGAGCTTT 962
Db 2003 GTGTACAAACCTTCCGATGGAACCTGATATTTCCATCCATCATCTCTGAGCTTT 2062
Qy 963 CGGAAATTCATAGGAGTGGGCTCAGCCGCTTCTCTGCTCAGTTTACTAGTGC 1022
Db 2063 CGGAAATTCATAGGAGTGGGCTCAGCCGCTTCTCTGCTCAGTTTACTAGTGC 2122
Qy 1023 ATTTGTCAGTGTGTTGAGGGCTTCCGCACTGTTTGGCTTCAATTATGATGAT 1082
Db 2123 ATTTGTCAGTGTGTTGAGGGCTTCCGCACTGTTTGGCTTCAATTATGATGAT 2182
Qy 1083 GTTGTACTGGGGCCAAAGTCTGTACACATCTTGAATCCGCTTTTACCGCTGTACCAAT 1142
Db 2183 GTTGTACTGGGGCCAAAGTCTGTACACATCTTGAATCCGCTTTTATACCGCTGTACCAAT 2242
Qy 1143 TTTCTTTTGTCTTTGGGTATACATTAAACCTTAATAA 1181
Db 2243 TTTCTTTTGTCTTTGGGTATACATTAAACCTTAATAA 2281

RESULT 9
US-09-718-095-8
; Sequence 8, Application US/09718095
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; APPLICANT: VAN GEYT, Sija
; APPLICANT: DE GENDT, Sija
; TITLE OF INVENTION: New HBV Sequences
; FILE REFERENCE: 2551-52
; CURRENT APPLICATION NUMBER: US/09/718.095
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: EP9870252.6
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US60/169.287
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PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1203
TYPE: DNA
ORGANISM: Hepatitis B virus
FEATURE:
NAME/KEY: variation
LOCATION: (33)..(35)
OTHER INFORMATION: unknown or other
NAME/KEY: variation
LOCATION: (161)
OTHER INFORMATION: unknown or other
US-09-718-095-8

Query Match 85.5%; Score 1010.2; DB 31; Length 1203;
Best Local Similarity 91.5%; Pred. No. 3.5e-286;
Matches 1069; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 3 GGGGAGAAATCTTCCAGCAGCATCTCTGGGATTCTTCCGACCAAGTTGGATCC 62
DB 36 GGGAAAGAACTTTCCAGCAGCATCTCTAGGATTCCTCCGATCAGCATGGACCC 95
QY 63 AGCTTCAGAGCAAAACCAACATCCAGATTGGGACTTCAATCCCAAGAGACCTG 122
DB 96 AGCATTCAGAGCAAAATACCAACATCCAGATTGGGACTTCAATCCCAAGAGACCTG 155
QY 123 GCGAAGCGCAACAGGTGAGCTGAGCATTCGGACTGGGGTTTACCCCGACGG 182
DB 156 GCGAAGCGCAACAGGTGAGCTGAGCATTCGGACTGGGGTTTACCCCGACGG 215
QY 183 AGGCTTTGGGGTGGAGGCTCAGGCTGAGGCAATACAAACCTTCCAGCAAAATCC 242
DB 216 AGGCTTTGGGGTGGAGGCTCAGGCTGAGGCAATACAAACCTTCCAGCAAAATCC 275
QY 243 GCGCTCTGCTCCAGCAATCGCAGTCAAGAAAGGAGCTTACCCGCTCTTCACTTT 302
DB 276 GCGCTCTGCTCCAGCAATCGCAGTCAAGAAAGGAGCTTACCCGCTCTTCACTTT 335
QY 303 GAGAAACACTCATCTCAAGCAGTCAAGTGAATCTCAACATTTCCACCAACTTCTGCA 362
DB 336 AAGAGCAGTCACTCTCAGGCGATGAGTGAATCTCAAGTCACTCAACAGTCTTACA 395
QY 363 AGATCCGAGTGAAGGTCTGATTTCCCTGCTGGTCTCAAGTCAAGTGAATTA 422
DB 396 AATCCCAAGTCAAGGAGGCTGATTTCCCTGCTGGTCTCAAGTCAAGTGAATTA 455
QY 423 CCTGCTCGACTACTGCTCTCCATATGTCATCTTCTGAGGATGGGAGCCCTGC 482
DB 456 CCTGCTCGACTACTGCTCTCCATATGTCATCTTCTGAGGATGGGAGCCCTGC 515
QY 483 GGGAAACATGAGAAATCATCATCAGATTCCTAGAGCCCTGCTGTTTCAAGCGGG 542
DB 516 ACCGAACATGAGAAATCATCATCAGATTCCTAGAGCCCTGCTGTTTCAAGCGGG 575
QY 543 GTTTTCTGTTGACAAAGATCTCAATACCGGAGTCTAGATCTGTGTGACTTC 602
DB 576 GTTTTCTGTTGACAAAGATCTCAATACCGGAGTCTAGATCTGTGTGACTTC 635
QY 603 TCTCAATTTCTAGGGGAACTACGCTGTCTTGGGCAAAATTCGAGTCCCAACCTC 662
DB 636 TCTCAATTTCTAGGGGAGTACGCTGTCTTGGGCAAAATTCGAGTCCCAACCTC 695
QY 663 CAATCACTGACCAACTCTGCTCTCAACTGCTGTTTACGCTGATGTGTCTGCG 722
DB 696 CAATCACTGACCAACTCTGCTCTCAACTGCTGTTTACGCTGATGTGTCTGCG 755
QY 723 GCGTTTATCATCTTCTCTTCACTCTGCTGATGCTCACTTTTGTGTGTTCTT 782
DB 756 GCGTTTATCATCTTCTCTTCACTCTGCTGATGCTCACTTTTGTGTGTTCTT 815
QY 783 GGAATATCAAGGATGTGCGGCTTGTCTCTAATTCAGGATCTTCAACCAAGCAGC 842

DB 816 GGAATATCAAGGATGTGCGGCTTGTCTCTAATTCAGGATCTTCAACCAAGCAGC 875
QY 843 GGGACCATGAGAGCTGACAGACTCTGCTCAAGAACTCTATGATATCCCTCTGTTG 902
DB 876 GGGACCTCGCAAAACCTTGACAGACTCTGCTCAAGAACTCTATGATATCCCTCTGTTG 935
QY 903 CTGTACAAACCTTGGATGGAATCTGACCTGTATTCATCCATCATCTGAGCTTT 962
DB 936 CTGTACAAACCTTGGATGGAATCTGACCTGTATTCATCCATCATCTGAGCTTT 995
QY 963 CGGAAATTCCTATGAGAGTGGGCTTCAAGCCGTTTCTTCCGCTCACTTACTAGTCC 1022
DB 996 CGGAAATTCCTATGAGAGTGGGCTTCAAGCCGTTTCTTCCGCTCACTTACTAGTCC 1055
QY 1023 ATTGTTCAGGTGCTGAGAGCTTCCCGCACTGTTGGCTTCACTATATGATGAT 1082
DB 1056 ATTGTTCAGGTGCTGAGAGCTTCCCGCACTGTTGGCTTCACTATATGATGAT 1115
QY 1083 GTTGTACTGGGGCCAGTCTGTACACCATCTTGTGCTTTTACCGCTGTACCAT 1142
DB 1116 GTTGTACTGGGGCCAGTCTGTACACCATCTTGTGCTTTTACCGCTGTACCAT 1175
QY 1143 TTTCTTTGCTCTTGGGATATATTTAA 1170
DB 1176 TTTCTTTGCTCTTGGGATATATTTAA 1203

RESULT 10
PCT-US02-32263-45
Sequence 45, Application PC/TUS0232263
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFeese, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bower, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5050WO
CURRENT APPLICATION NUMBER: PCT/US02/32263
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/334,301
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 1203
TYPE: DNA
ORGANISM: Hepatitis B virus
PCT-US02-32263-45

Query Match 85.1%; Score 1005.2; DB 1; Length 1203;
Best Local Similarity 91.2%; Pred. No. 1e-284;
Matches 1067; Conservative 0; Mismatches 103; Indels 0; Gaps 0;


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QY 361 CAAGATCCAGAGTAGAGGTCTGATTTCCCTGCTGAGGCTCAGTTTCAGAAACAGTA 420
DB 394 CTAGATCCAGAGTAGAGGCTCTATATTTTCCGCTGGTGGCTCCAGTTCCGGAACAGTA 453
QY 421 AACCTGTTCCGACTACTCTCTCTCCGATATGTCATTTTCCGAGATTGGGACCTT 480
DB 454 AACCTGTTCCGACTACTCTCTCCGATATGTCATTTTCCGAGATTGGGACCTT 513
QY 481 GCGGGAACATGAGAAACATCAATCAGATTCTGAGACCCCTGCTGTTTACAGGCG 540
DB 514 GCACCGAACATGAGAAACATCAGATTCTGAGACCCCTGCTGTTTACAGGCG 573
QY 541 GGGTTTTCTTGTGACAGAAATCTCAGAAATACCGAGATCTAGACTGATGAGT 600
DB 574 GGGTTTTCTTGTGACAGAAATCTCAGAAATACCGAGATCTAGACTGATGAGT 633
QY 601 TCTCTCAATTTTCTTAGGGGAACTACCGTGTCTTGGCCAAATTTGCAATGCCAAC 660
DB 634 TCTCTCAATTTTCTTAGGGGAGACCCAGTGTCTGCGCAAAATTTGCAATGCCAAC 693
QY 661 TCCAACTCACTACCAACCTCTGTCTCAGCTTGTCTGATGCTGATGCTGATGCTG 720
DB 694 TCCAACTCACTACCAACCTCTGTCTCAGCTTGTCTGATGCTGATGCTGATGCTG 753
QY 721 CGGCGTTTATCATCTTCTCTTCACTCTGCTGATGCTGATGCTGATGCTGATGCTG 780
DB 754 CGGCGTTTATCATCTTCTCTTCACTCTGCTGATGCTGATGCTGATGCTGATGCTG 813
QY 781 CTGGAATCAATCAAGTATGTTGCCCGTTTGTCTCTAATTCAGAGATCTTCAACAC 840
DB 814 CTGGAATCAATCAAGTATGTTGCCCGTTTGTCTCTAATTCAGAGATCTTCAACAC 873
QY 841 ACGGAGCAATGAGAGGCTGAGAGCTGCTGCTCAAGGAACTCTATGATCCCTGCTG 900
DB 874 ACGGAGCAATGAGAGGCTGAGAGCTGCTGCTCAAGGAACTCTATGATCCCTGCTG 933
QY 901 TGCCTGACAAAACCTTCGAGTGAAGAACTGCACTGATCCCATCCATCATCTGAGCT 960
DB 934 TGCCTGACAAAACCTTCGAGTGAAGAACTGCACTGATCCCATCCATCATCTGAGCT 993
QY 961 TTGGGAAATTCCTATGAGAGTGGGCTCAGCCCGTTTCTCTGCTCAGTTTACTAGT 1020
DB 994 TTGGGAAATTCCTATGAGAGTGGGCTCAGCCCGTTTCTCTGCTCAGTTTACTAGT 1053
QY 1021 CCATTGTTCACTGTTGCTGAGGCTTTCCCACTGTTGCTTCACTATATGAGT 1080
DB 1054 CCATTGTTCACTGTTGCTGAGGCTTTCCCACTGTTGCTTCACTATATGAGT 1113
QY 1081 ATGTGTAATGAGGAGCAAGTCTGTACACCATCTGAGTCCCTTTTACCGCTTACCA 1140
DB 1114 ATGTGTAATGAGGAGCAAGTCTGTACACCATCTGAGTCCCTTTTACCGCTTACCA 1173
QY 1141 ATTTTCTTTTGTCTTGGGTATACATTAA 1170
DB 1174 ATTTTCTTTTGTCTTGGGTATACATTGA 1203

RESULT 12
US-10-410-897-45
; Sequence 45, Application US/10410897
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hayes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: FACTOR IX: REMODELING AND GLYCOSYLATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523

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; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-410-897-45

Query Match      85.1%; Score 1005.2; DB 52; Length 1203;
Best Local Similarity 91.2%; Pred. No. 1e-284;
Matches 1067; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1 ATGGGGCAAGATCTTCCACAGCAATCCTGAGGATCTTCCGACACAGTTGAT 60
DB 34 ATGGGCAAGATCTTCTGTTCTCCAAATCTCTGGGATCTTCCGATCACAGTTGAC 93
QY 61 CCAGCTTCAGAGCAACCAACCAATCCAGATTGGACTTCAATCCCAACAGACACC 120
DB 94 CCGGCTTCAGAGCAACCAACCAATCCAGATTGGACTTCAATCCCAACAGATCAC 153
QY 121 TGGCCAGAGCCCAACAGATGAGCTGAGCATTCGACTGGGGTTACCCACCGCAC 180
DB 154 TGGCCAGAGCCCAACAGATGAGCTGAGCATTCGAGCATTCGAGCATTCACACAC 213
QY 181 GGAGGCTTTTGGGGTGGAGGCTTCAGGCTCAGGAGCAATACCAAACTTTGCACAAT 240
DB 214 GGAGGCTTTTGGGGTGGAGGCTTCAGGCTCAGGAGCAATACCAAACTTTGCACAAG 273
QY 241 CCGGCTTCGCTTCACCAATTCGAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 274 CCGGCTTCGCTTCACCAATTCGAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 333
QY 301 TTGAGAAACATCATCTCAAGCCATGAGTGAATCTCACAACTTTTCACCAACCTCTG 360
DB 334 CTAGAGAGACATCATCTCAAGCCATGAGTGAATCTCACAACTTTTCACCAACCTCTG 393
QY 361 CAAGATCCAGAGTAGAGGTCTGATTTCCCTGCTGAGGCTCCAGTTTCAGAAACAGTA 420
DB 394 CTAGATCCAGAGTAGAGGTCTGATTTCCCTGCTGAGGCTCCAGTTTCAGAAACAGTA 453
QY 421 AACCTGTTCCGACTACTGTCTCTCCATATGTCATTTTCCGAGATTGGGACCTT 480
DB 454 AACCTGTTCCGACTACTGTCTCTCCATATGTCATTTTCCGAGATTGGGACCTT 513
QY 481 GCGGGAACATGAGAAACATCAATCAGATTCTGAGACCCCTGCTGTTTACAGGCG 540
DB 514 GCACCGAACATGAGAAACATCAGATTCTGAGACCCCTGCTGTTTACAGGCG 573
QY 541 GGGTTTTCTTGTGACAGAAATCTCAGAAATACCGAGATCTAGACTGATGAGT 600
DB 574 GGGTTTTCTTGTGACAGAAATCTCAGAAATACCGAGATCTAGACTGATGAGT 633
QY 601 TCTCTCAATTTTCTTAGGGGAACTACCGTGTCTTGGCCAAATTTGCAATGCCAAC 660
DB 634 TCTCTCAATTTTCTTAGGGGAGACCCAGTGTCTGCGCAAAATTTGCAATGCCAAC 693
QY 661 TCCAACTCACTACCAACCTCTGTCTCAGCTTGTCTGATGCTGATGCTGATGCTG 720
DB 694 TCCAACTCACTACCAACCTCTGTCTCAGCTTGTCTGATGCTGATGCTGATGCTG 753

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QY 721 CGGCGTTTATCATCTTCTCTTCATCTCTGCTATGCTCATCTTCTTGTTGTTCTT 780
| | | | |
Db 754 CGGCGTTTATCATCTTCTCTTCATCTCTGCTATGCTCATCTTCTTGTTGTTCTT 813
| | | | |
QY 781 CTGAGCATATCAAGTATGTTGCCGTTTGTCTCTAATTCAGAGATTTCAACACGAGC 840
| | | | |
Db 814 CTGAGCATATCAAGTATGTTGCCGTTTGTCTCTAATTCAGAGATTTCAACACGAGC 873
| | | | |
QY 841 ACGGAGCATATGAGAGCTGACGACTCTGCTCAAGAACTCTATGTAATCCCTCTGT 900
| | | | |
Db 874 ACGGAGCATATGAGAGCTGACGACTCTGCTCAAGAACTCTATGTAATCCCTCTGT 933
| | | | |
QY 901 TGGCTATCAAAACCTTTCGATGAGAACTGACCTGTAATCCATCCCATCATCTGGGCT 960
| | | | |
Db 934 TGGCTATCAAAACCTTTCGATGAGAACTGACCTGTAATCCATCCCATCATCTGGGCT 993
| | | | |
QY 961 TTGGGAAAATTTCTATGAGAGTGGGCTCAGCCCGTTTCTCTGCTCACTTTACTAGTG 1020
| | | | |
Db 994 TTGGCAAGATTTCTATGAGAGTGGGCTCAGTCCGTTTCTCTGCTCACTTTACTAGTG 1053
| | | | |
QY 1021 CCAATTTGTCAGTGTCTGATGAGGCTTTCCGCCCACTGTTGGCTTTCAGTTATATGATG 1080
| | | | |
Db 1054 CCAATTTGTCAGTGTCTGATGAGGCTTTCCGCCCACTGTTGGCTTTCAGTTATATGATG 1113
| | | | |
QY 1081 ATGTTGACTGGGGGCCAAGTCTGTACACCATCTTGAGTCCCTTTTACCGCTGTTACCA 1140
| | | | |
Db 1114 ATGTTGATGGGGGCCAAGTCTGTACACCATCTTGAGTCCCTTTTACCTTATATACCA 1173
| | | | |
QY 1141 ATTTTCTTTTGTCTTTGGGTATATATTAA 1170
| | | | |
Db 1174 ATTTTCTTTTGTCTTTGGGTATATATTGA 1203
| | | | |

RESULT 13

US-10-410-913-45
; Sequence 45, Application US/10410913
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Howe, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410, 913
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-410-913-45

Query Match 85.1%; Score 1005.2; DB 52; Length 1203;
Best Local Similarity 91.2%; Pred. No. 1e-284;

Matches 1067; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 1 ATGGGCAAGAAATTTTCCACAGCAATCTCTGGGATTTCTTCCGACCAAGTTGAT 60
| | | | |
Db 34 ATGGGCAAGAAATTTTCTGTCTCCATCTCTGGGATTTCTTCCGATACCAAGTTGGAG 93
| | | | |
QY 61 CGAGCTTCAAGAGCAAAACCAACATTCAGATTTGGAGCTTCAATCCCAAGAGACCC 120
| | | | |
Db 94 CTGGCTTGGAGCCAACTCAAAACATTCAGATTTGGAGCTTCAATCCCAAGAGATCAC 153
| | | | |
QY 121 TGGCCAGAGCCCAAGAGATGAGAGATTTGGAGCTGGGGTTACCCCAAGCCGAC 180
| | | | |
Db 154 TGGCCAGAGCAATCAAGATGAGAGAGGAGACTTGGGCAAGGTTCAACCCACACAC 213
| | | | |
QY 181 GAGAGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGATTAACAAACCTTGGCCAGCAAT 240
| | | | |
Db 214 GGGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGATTAATGACAAAGTCCAGAGAGG 273
| | | | |
QY 241 CGGCTCTGCTTCCACCAATGCGCAGTCAAGAGGAGAGCTTACCCGCTGTCTCACT 300
| | | | |
Db 274 CTTCTCTGTTTCCACCAATGCGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 333
| | | | |
QY 301 TTGAGAAACATCATCTCAAGGATGAGAGAGTCAAGAGAGTTCACCAACTTCAACCA 360
| | | | |
Db 334 CTAGAGAGAGATCATCTCAAGGATGAGAGAGTCAAGAGAGTTCACCAACTTCAACCA 393
| | | | |
QY 361 CAAGATCCCAAGAGTGAAGGCTGTATTTCCCTGCTGAGTGTCTCAAGTTCAGAGAGAG 420
| | | | |
Db 394 CTAGATCCCAAGAGTGAAGGCTGTATTTCCCTGCTGAGTGTCTCAAGTTCAGAGAGAG 453
| | | | |
QY 421 AACCTGTTCGACTACTGTCTCTCCATATGCTCAATCTTCTCGAGATTTGGGACCT 480
| | | | |
Db 454 AACCTGTTCGACTACTGTCTCTCCATATGCTCAATCTTCTCGAGAGAGTGGGACCT 513
| | | | |
QY 481 GCGGGAACAATGAGAGACATCATGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAG 540
| | | | |
Db 514 GCAACCAACATGAGAGAGACATCATGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAG 573
| | | | |
QY 541 GGGTTTTTCTGTTGACAAAGATCTCACAAATACCGCAGAGTCAAGTCTGAGTGAAGT 600
| | | | |
Db 574 GGGTTTTTCTGTTGACAAAGATCTCACAAATACCGCAGAGTCAAGTCTGAGTGAAGT 633
| | | | |
QY 601 TCTCTCAATTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 660
| | | | |
Db 634 TCTCTCAATTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 693
| | | | |
QY 661 TCCAAATCATCAGCAACCTCTCTCTCCAACTTCTGCTGATATGCTGAGATGTCG 720
| | | | |
Db 694 TCCAAATCATCAGCAACCTCTCTCTCCAACTTCTGCTGATATGCTGAGATGTCG 753
| | | | |
QY 721 CGGCGTTTATCATCTTCTCTTCATCTGCTCTGATGCTCACTTCTTGTTGTTCTT 780
| | | | |
Db 754 CGGCGTTTATCATCTTCTCTTCATCTGCTCTGATGCTCACTTCTTGTTGTTCTT 813
| | | | |
QY 781 CTGAGCATATCAAGTATGTTGCCGTTTGTCTCTAATTCAGAGATTTCAACACGAGC 840
| | | | |
Db 814 CTGAGCATATCAAGTATGTTGCCGTTTGTCTCTAATTCAGAGATTTCAACACGAGC 873
| | | | |
QY 841 ACGGAGCATATGAGAGCTGACGACTCTGCTCAAGAACTCTATGTAATCCCTCTGT 900
| | | | |
Db 874 ACGGAGCATATGAGAGCTGACGACTCTGCTCAAGAACTCTATGTAATCCCTCTGT 933
| | | | |
QY 901 TGGCTATCAAAACCTTTCGATGAGAACTGACCTGTAATCCATCCCATCATCTGGGCT 960
| | | | |
Db 934 TGGCTATCAAAACCTTTCGATGAGAACTGACCTGTAATCCATCCCATCATCTGGGCT 993
| | | | |
QY 961 TTGGGAAAATTTCTATGAGAGTGGGCTCAGCCCGTTTCTCTGCTCACTTTACTAGTG 1020
| | | | |
Db 994 TTGGCAAGATTTCTATGAGAGTGGGCTCAGTCCGTTTCTCTGCTCACTTTACTAGTG 1053
| | | | |
QY 1021 CCAATTTGTCAGTGTCTGATGAGGCTTTCCGCCCACTGTTGGCTTTCAGTTATATGATG 1080
| | | | |
Db 1054 CCAATTTGTCAGTGTCTGATGAGGCTTTCCGCCCACTGTTGGCTTTCAGTTATATGATG 1113
| | | | |

QY 1081 ATGTGTACGCGGCGCAAGTCTGTACACCAATCTTGTAGTCCCTTTTACCGGTGTTACCA 1140
| | | | |
DB 1114 ATGTGTATGGGGGCGCAAGTCTGTACACCAATCTTGTAGTCCCTTTTACCTGTATTACCA 1173
| | | | |
QY 1141 ATTTCTTTGCTTGTGGGTATACATTAA 1170
| | | | |
DB 1174 ATTTCTTTGCTTGTGGGTATACATTGA 1203
| | | | |
RESULT 14
US-10-410-930-45
; Sequence 45, Application US/10410930
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: BETA
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410, 930
; PRIOR APPLICATION NUMBER: US 60/328, 523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344, 692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387, 292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391, 777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396, 594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404, 249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407, 527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-410-930-45
Query Match 85.1%; Score 1005.2; DB 52; Length 1203;
Best Local Similarity 91.2%; Pred. No. 1e-284;
Matches 1067; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

DB 334 CTAAAGACAGTCTCTAGGCGCATGACGTGAAGTCCACAACAATTCCACCAAGCTCTG 393
| | | | |
QY 361 CAAGATCCCAAGGTAGAGGTGTATTTCCCTGCTGGTGGTCCAGTTACAGAAACATG 420
| | | | |
DB 394 CTAGATCCCAAGGTAGAGGTGTATTTCCCTGCTGGTGGTCCAGTTACAGAAACATG 453
| | | | |
QY 421 AACCTGTTCCGACTACTGTCTCTCCATATGCTCAATCTTTCGAGATGAGGAGCCCT 480
| | | | |
DB 454 AACCTGTTCCGACTACTGTCTCTCCATATGCTCAATCTTTCGAGATGAGGAGCCCT 513
| | | | |
QY 481 GCGCGAATCATGAGAACATCATCAGATTCCTAGAACCCCTCTCTGTTTACAGGCG 540
| | | | |
DB 514 GCACCGAATCATGAGAACATCATCAGATTCCTAGAACCCCTCTCTGTTTACAGGCG 573
| | | | |
QY 541 GGGTTTTCTTTGTGACAAAGATCTCTACAAATACCGCAGAGTGTAGTCTGTTGAGT 600
| | | | |
DB 574 GGGTTTTCTTTGTTTACAAAGATCTCTCAAAATACCAAGAGTGTAGTCTGTTGAGT 633
| | | | |
QY 601 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCAAAATTCGAGTCCCAACC 660
| | | | |
DB 634 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCAAAATTCGAGTCCCAACC 693
| | | | |
QY 661 TCCAATCACTACCAACCTCTGTCTCTCAACTTGTCTGTTATCGTGAATGTGTCTG 720
| | | | |
DB 694 TCCAATCACTACCAACCTCTGTCTCTCAACTTGTCTGTTATCGTGAATGTGTCTG 753
| | | | |
QY 721 CGCGTTTTATATCTTCTCTTCAATCTCTGCTGTATGCTGTATCTTCTGTTGTTCTT 780
| | | | |
DB 754 CGCGTTTTATATCTTCTCTTCAATCTCTGCTGTATGCTGTATCTTCTGTTGTTCTT 813
| | | | |
QY 781 CTGACATCAAGATGATGCGCGTGTCTCTCAATTTCCAGATCTTCAACCAACCAC 840
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DB 814 CTGACATCAAGATGATGCGCGTGTCTCTCAATTTCCAGATCTTCAACCAACCAC 873
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QY 841 ACGGACCATGAGAGGCTGTGACGATCTCTGCTCAAGAACTCTATGATCTCTCTGT 900
| | | | |
DB 874 ACGGACCATGAGAGGCTGTGACGATCTCTGCTCAAGAACTCTATGATCTCTCTGT 933
| | | | |
QY 901 TGTCTTACAAAACCTTTCGATGAGAAATGACATCTGTATTCCTATCCATCATCTGGCT 960
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DB 934 TGTCTTACAAAACCTTTCGATGAGAAATGACATCTGTATTCCTATCCATCATCTGGCT 993
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QY 961 TTGGAAATTCCTATGAGAGGCTGTGACGATCTCTGCTCAAGAACTCTATGATCTCTGT 1020
| | | | |
DB 994 TTGGAAATTCCTATGAGAGGCTGTGACGATCTCTGCTCAAGAACTCTATGATCTCTGT 1053
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QY 1021 CCATTGTTCAAGTGTGTGAGGCTTCCCACTGTTGGCTTCAATTATGATG 1080
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DB 1054 CCATTGTTCAAGTGTGTGAGGCTTCCCACTGTTGGCTTCAATTATGATG 1113
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QY 1081 ATGTGTACGCGGCGCAAGTCTGTACACCAATCTTGTAGTCCCTTTTACCGGTGTTACCA 1140
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DB 1114 ATGTGTATGGGGGCGCAAGTCTGTACACCAATCTTGTAGTCCCTTTTACCTGTATTACCA 1173
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QY 1141 ATTTCTTTGCTTGTGGGTATACATTAA 1170
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DB 1174 ATTTCTTTGCTTGTGGGTATACATTGA 1203
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RESULT 15
US-10-410-945-45
; Sequence 45, Application US/10410945
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083


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; CURRENT APPLICATION NUMBER: US/10/410,945
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 45
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-410-945-45

Query Match      85.1%; Score 1005.2; DB 52; Length 1203;
Best Local Similarity 91.2%; Pred. No. 1e-284;
Matches 1067; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY      1 ATGGGCGAAGATCTTTCCACGAGCAATCTCTGGGATTTCTTCCCGACCAAGTTGGAT 60
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DB      94 CTGCGCTTGGAGCCCAACTCAACATCCAGATTGGGACTTCAACCCCAACAGAGATCAC 153
QY      121 TGGCCAGAGCCCAACAGAGTAGAGAGCTGAGCAATTCGGAATGGGGTTACCCCAACCGCAC 180
DB      154 TGGCCAGAGGCAATCAAGGTAGAGCGGAGACTTCGGGCCAGGGTTCAACCCCAACGAC 213
QY      181 GAGAGCCTTTTGGGGTGGAGACCTCTCAGGCTCAGGGGCTTAACAAACCTTGGCAAGCAAT 240
DB      214 GGGGGCTTTTGGGGTGGAGACCTCTCAGGCTCAGGGGCTTAATGACAAAGTGCAGGCG 273
QY      241 CCGCCTCTCTCTTCCACCAATCGCCAGTCAAGAGCAAGCAAGCCCTACCCCGCTGTCTCACT 300
DB      274 CTCTCTCTCTTTCACCAATCGGCACTCAGGAAGACAGCTACTCTCCACTCTCTCACT 333
QY      301 TTGAGAAACATCATCTCAAGCCATGAGTGAATCCACAACTTTCACCAAACTCTG 360
DB      334 CTAAAGAGACAGTCACTCTCAGGCAATGAGTGAATCCACAACTTTCACCAAGCTCTG 393
QY      361 CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGTGGTCCAGTTCAAGAAACGTA 420
DB      394 CTAGATCCAGAGTGAAGGTCTGTATTTCTGCTGTGGTCCAGTTCCGGAACGTA 453
QY      421 AACCTGTTCGACTACTGTCTCTCCCATATCGTCAATCTTCTGAGAGATTGGGACCT 480
DB      454 AACCTGTTCGACTACTGTCTCTCCCATATCGTCAATCTTCTGAGAGACTGGGACCT 513
QY      481 GCGGGAACATGAGAACATCATCAGATTCCTAGAGACCCCTGCTGTGTTCAGAGCG 540
DB      514 GCACGGAACATGAGAGACCAACATCAGGATTCCTAGAGACCCCTGCTGTGTTCAGAGCG 573
QY      541 GGGTTTTTCTTTGAGCAAGATCTCTCAATATCCGAGAGTCTAGACTGTGTGACT 600
DB      574 GGGTTTTTCTTTGAGCAAGATCTCTCAATATCCAGAGTCTAGACTGTGTGACT 633
QY      601 TCTCTCAATTTTCTAGGGGAACTACCGTGTGTCTTGGCCAAATTCGAGTCCCAACC 660
DB      634 TCTCTCAATTTTCTAGGGGAGACCAAGTGTGTCTTGGCCAAATTCGAGTCCCAACC 693
QY      661 TCGAATCATTCACCAACTCTCTGTCTTCAACTTGTCTGTGTTATCGCTGGAATGTCTG 720
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DB      694 TCGAATCATTCACCAACTCTCTGTCTTCAACTTGTCTGTGTTATCGCTGGAATGTCTG 753
QY      721 CGGCGTTTATCATCTTCCCTTCATCTGCTGCTATAGCTCATCTTCTTGTGTTCTT 780
DB      754 CGGCGTTTATCATCTTCCCTTCATCTGCTGCTATAGCTCATCTTCTTGTGTTCTT 813
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DB      814 CTGACATCAAGATATGTTGCCGTTTGTCTTATTCAGAGATCTTCAACCAACGAC 873
QY      841 ACGGAGCATGCAAGCTGCAAGATCTCTGCTCAAGAACTCTATATCTCTCTCT 900
DB      874 ACGGAGCATGCAAGCTGCAAGATCTCTGCTCAAGAACTCTATATCTCTCTCT 933
QY      901 TGCTGTACAAACCTTCGAGTGAAGCTGCAACCTGTATTCATCCATCATCTGGGCT 960
DB      934 TGCTGTACAAACCTTCGAGTGAAGCTGCAACCTGTATTCATCCATCATCTGGGCT 993
QY      961 TTGGAAAAATTCCTATGGAGTGGGCTGAGCCGTTTCTCTGCTCAAGTTACTAGTG 1020
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DB      1054 CCATTGTTCAAGTGTTCCTAGGCTTTCCCACTGTTTGGCTTCACTTATATGATG 1113
QY      1081 ATGTTGACGGGGGCAAGTCTGTACACCATCTTGAATCCCTTTTACCGCTGTACCA 1140
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OW nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810.8	68.7	846	6 US-10-383-317-11	Sequence 11, Appl
2	756.4	64.0	846	6 US-10-383-317-9	Sequence 9, Appl
3	710.8	60.2	1977	1 PCT-US03-18993-97	Sequence 15, Appl
4	412	34.9	849	6 US-10-383-317-15	Sequence 1, Appl
5	124.8	10.6	128	1 PCT-US03-18993-1	Sequence 68, Appl
6	88.2	7.5	93	1 PCT-US03-18993-68	Sequence 69, Appl
7	71.4	6.0	73	1 PCT-US03-18993-69	Sequence 67, Appl
8	69.4	5.9	71	1 PCT-US03-18993-67	Sequence 95, Appl
9	57.4	4.9	59	1 PCT-US03-18993-95	Sequence 7, Appl
10	53.8	4.6	57	6 US-10-388-918A-7	Sequence 84, Appl
11	50.8	4.3	54	1 PCT-US03-18993-4	Sequence 74, Appl
12	50	4.2	50	1 PCT-US03-18993-84	Sequence 78, Appl
13	48.4	4.1	50	1 PCT-US03-18993-2	Sequence 142, App
14	43	3.6	45	1 PCT-US03-18993-78	Sequence 83, Appl
15	42.8	3.6	46	1 PCT-US03-18993-142	Sequence 74, Appl
16	42	3.6	42	1 PCT-US03-18993-83	Sequence 77, Appl
17	40	3.4	40	1 PCT-US03-18993-74	Sequence 16509, A
18	40	3.4	40	1 PCT-US03-18993-77	Sequence 175, App
19	38	3.2	23261	7 US-60-495-114-16509	Sequence 3692, Ap
20	38	3.2	96592	1 PCT-US02-36071A-175	Sequence 90, Appl
21	37.6	3.2	58398	7 US-60-495-135-3692	Sequence 38006, A
22	37.4	3.2	39	1 PCT-US03-18993-90	Sequence 38007, A
23	36.8	3.1	201	7 US-60-495-114-38006	Sequence 38009, A
24	36.8	3.1	201	7 US-60-495-114-38007	Sequence 19270, A
25	36.8	3.1	201	7 US-60-495-114-38009	
26	36.8	3.1	16701	7 US-60-487-610-19270	

C 27	36.8	3.1	57978	7 US-60-487-610-19974	Sequence 19974, A
C 28	36.8	3.1	384485	7 US-60-495-114-16382	Sequence 16382, A
C 29	36.2	3.1	3379	7 US-60-487-610-1316	Sequence 1316, Ap
C 30	36.2	3.1	3379	7 US-60-485-450-843	Sequence 843, App
C 31	36	3.0	36	1 PCT-US03-18993-70	Sequence 70, Appl
C 32	36	3.0	36	1 PCT-US03-18993-82	Sequence 82, Appl
C 33	36	3.0	1072	7 US-60-493-007-3096	Sequence 3096, Ap
C 34	35.4	3.0	27587	1 PCT-US02-38582-253	Sequence 253, App
C 35	35.4	3.0	52846	7 US-60-487-610-19654	Sequence 19654, A
C 36	35.4	3.0	13831263	5 US-09-947-914-41	Sequence 41, Appl
C 37	35.2	3.0	2037	6 US-10-425-114A-26697	Sequence 26697, A
C 38	35.2	3.0	13208	7 US-60-487-610-19923	Sequence 19923, A
C 39	35.2	3.0	13831263	5 US-09-947-914-41	Sequence 41, Appl
C 40	35	3.0	35	1 PCT-US03-18993-89	Sequence 89, Appl
C 41	35	3.0	35	1 PCT-US03-18993-92	Sequence 92, Appl
C 42	35	3.0	35	1 PCT-US03-18993-126	Sequence 126, App
C 43	35	3.0	30400	7 US-60-487-610-19473	Sequence 19473, A
C 44	34.8	2.9	923	6 US-10-425-114A-30410	Sequence 30410, A
C 45	34.8	2.9	927	6 US-10-425-114A-31990	Sequence 31990, A

ALIGNMENTS

RESULT 1
US-10-383-317-11
Sequence 11, Application US/10383317
GENERAL INFORMATION:
APPLICANT: Punnonen, Juh
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/10/383,317
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/247,890
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 846
TYPE: DNA
ORGANISM: Hepatitis B virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(846)
OTHER INFORMATION: Pres2-S coding region of hepatitis B virus ayw
OTHER INFORMATION: surface antigen (HBsAg)
US-10-383-317-11

Query Match 68.7%; Score 810.8; DB 6; Length 846;
Best Local Similarity 97.4%; Pred. No. 3.4e-254;
Matches 824; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 325 ATGCGTGAATCCACAACTTCCACCAATCTGCAAGATCCAGAGTGAGAGTCG 384
DB 1 ATGCGTGAATCCACAACTTCCACCAATCTGCAAGATCCAGAGTGAGAGTCG 60
QY 385 TATTTCCCTGCTGCTGCTCCAGTTCCAGAAACAGTAACCTCTGCTCACTACTCTCT 444
DB 61 TATTTCCCTGCTGCTGCTCCAGTTCCAGAAACAGTAACCTCTGCTCACTACTCTCT 120
QY 445 CCCATATGTCATCTTTCTCGAGATTGGGACCTCGCGGAGATGAGAACTCACA 504
DB 121 CCTTATGTCATCTTTCTCGAGATTGGGACCTCGCGGAGATGAGAACTCACA 180

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QY 505 TCAGATTCCTAGGACCCCTGCTGCTGTATACAGCGCGGCTTTTCTTGTGACAGATC 564
DB 181 TCAGATTCCTAGGACCCCTGCTGCTGTATACAGCGCGGCTTTTCTTGTGACAGATC 240
QY 565 CTCACATACCGAGAGCTAGACTCGTGGGACCTCTCTCAATTTTCTAGGGGAACT 624
DB 241 CTCACATACCGAGAGCTAGACTCGTGGGACCTCTCTCAATTTTCTAGGGGAACT 300
QY 625 ACCGTGTGCTGGCCAAATTCGACGTCCCAACCTCAATCACTGACCAACCTCTGT 684
DB 301 ACCGTGTGCTGGCCAAATTCGACGTCCCAACCTCAATCACTGACCAACCTCTGT 360
QY 685 CTTCCAACTGCTGCTGTATCGTGGATGTGTGCGGGCTTTATCACTTCTCTTC 744
DB 361 CTTCCAACTGCTGCTGTATCGTGGATGTGTGCGGGCTTTATCACTTCTCTTC 420
QY 745 ATCTGTGCTATGACCTCATCTCTTGTGTTCTTGACATCAAGGATGTGCCC 804
DB 421 ATCTGTGCTATGACCTCATCTCTTGTGTTCTTGACATCAAGGATGTGCCC 480
QY 805 GTTGTCTCTTAATTCAGGATCTTCAACGACGAGACCGGACCATGACAGCCTGACG 864
DB 481 GTTGTCTCTTAATTCAGGATCTTCAACGACGAGACCGGACCATGACAGCCTGACG 540
QY 865 ACTCTGCTCAAGGAACTCTATGTATCCTCTCTGCTGTACAAAACCTTGGATGA 924
DB 541 ACTCTGCTCAAGGAACTCTATGTATCCTCTCTGCTGTACAAAACCTTGGATGA 600
QY 925 AACTGACCTGTATTCCTCATCCCATCATCTGAGGCTTGGGAAAATTCATATGGAATGG 984
DB 601 AACTGACCTGTATTCCTCATCCCATCATCTGAGGCTTGGGAAAATTCATATGGAATGG 660
QY 985 GCCTGACCCGCTTCTCTGAGCTCACTTACAGTTCATTTGTTCAAGTTCGATGG 1044
DB 661 GCCTGACCCGCTTCTCTGAGCTCACTTACAGTTCATTTGTTCAAGTTCGATGG 720
QY 1045 CTTTCCCCCACTGTTGGCTTTCAGTATATGATATGTTTACTGGGGCCCAAGCTG 1104
DB 721 CTTTCCCCCACTGTTGGCTTTCAGTATATGATATGTTTACTGGGGCCCAAGCTG 780
QY 1105 TACACATCTTGAGTCCCTTTTACCGCTGTACCAATTTCTTTTGTGGGTATAC 1164
DB 781 TACACATCTTGAGTCCCTTTTACCGCTGTACCAATTTCTTTTGTGGGTATAC 840
QY 1165 ATTTAA 1170
DB 841 ATTTAA 846

RESULT 2
US-10-383-317-9
; Sequence 9, Application US/10383317
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juha
; APPLICANT: Baes, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/10/383,317
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 846
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; TYPE: DNA
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(846)
; OTHER INFORMATION: PreS2-S coding region of hepatitis B virus adr
; OTHER INFORMATION: surface antigen (HBsAg)
US-10-383-317-9

Query Match          64.0%; Score 756.4; DB 6; Length 846;
Best Local Similarity 93.4%; Pred. No. 2e-236;
Matches 790; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 325 ATGCAAGTGAATCTCCAACTTTCCACCAATCTGCAAGATCCGAGTGAAGTCTG 384
DB 1 ATGCAAGTGAATCTCCAACTTTCCACCAATCTGCAAGATCCGAGTGAAGTCTG 60
QY 385 TATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
DB 61 TATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 445 CCCATATCGTCAATCTTCTGAGAGATTTGGGACCTGCGCGGAATGAGAAATCACA 504
DB 121 CCCATATCGTCAATCTTCTGAGAGATTTGGGACCTGCGCGGAATGAGAAATCACA 180
QY 505 TCAGATTCCTAGGACCCCTGCTGCTGTATACAGCGCGGCTTTTCTTGTGACAAATC 564
DB 181 TCAGATTCCTAGGACCCCTGCTGCTGTATACAGCGCGGCTTTTCTTGTGACAAATC 240
QY 565 CTCACAAATACCGAGAGTCTAGACTCGTGGTGAATCCCTGCTGACCTGCTGCTGCTG 624
DB 241 CTCACAAATACCGAGAGTCTAGACTCGTGGTGAATCCCTGCTGACCTGCTGCTGCTG 300
QY 625 ACCGTGTGCTGGCCAAATTCGACGTCCCAACCTCAATCACTGACCAACCTCTGT 684
DB 301 ACCGTGTGCTGGCCAAATTCGACGTCCCAACCTCAATCACTGACCAACCTCTGT 360
QY 685 CTTCCAACTGCTGCTGTATCGTGGATGTGTGCGGGCTTTATCACTTCTCTTC 744
DB 361 CTTCCAACTGCTGCTGTATCGTGGATGTGTGCGGGCTTTATCACTTCTCTTC 420
QY 745 ATCTGTGCTATGACCTCATCTCTTGTGTTCTTGACATCAAGGATGTGCCC 804
DB 421 ATCTGTGCTATGACCTCATCTCTTGTGTTCTTGACATCAAGGATGTGCTC 480
QY 805 GTTGTCTCTTAATTCAGGATCTTCAACGACGAGACCGGACCATGACAGCCTGACG 864
DB 481 GTTGTCTCTTAATTCAGGATCTTCAACGACGAGACCGGACCATGACAGCCTGACG 540
QY 865 ACTCTGCTCAAGGAACTCTATGTATCCTCTCTGCTGTACAAAACCTTGGATGA 924
DB 541 ACTCTGCTCAAGGAACTCTATGTATCCTCTCTGCTGTACAAAACCTTGGATGA 600
QY 925 AACTGACCTGTATTCCTCATCCCATCATCTGAGGCTTGGGAAAATTCATATGGAATGG 984
DB 601 AACTGACCTGTATTCCTCATCCCATCATCTGAGGCTTGGGAAAATTCATATGGAATGG 660
QY 985 GCCTGACCCGCTTCTCTGAGCTCACTTACAGTTCATTTGTTCAAGTTCGATGG 1044
DB 661 GCCTGACCCGCTTCTCTGAGCTCACTTACAGTTCATTTGTTCAAGTTCGATGG 720
QY 1045 CTTTCCCCCACTGTTGGCTTTCAGTATATGATATGTTTACTGGGGCCCAAGCTG 1104
DB 721 CTTTCCCCCACTGTTGGCTTTCAGTATATGATATGTTTACTGGGGCCCAAGCTG 780
QY 1105 TACACATCTTGAGTCCCTTTTACCGCTGTACCAATTTCTTTTGTGGGTATAC 1164
DB 781 TACACATCTTGAGTCCCTTTTACCGCTGTACCAATTTCTTTTGTGGGTATAC 840
QY 1165 ATTTAA 1170
DB 841 ATTTAA 846
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RESULT 3
PCT-US03-18993-97
; Sequence 97, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI34-02 UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 97
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-97
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Query Match      60.2%; Score 710.8; DB 1; Length 1977;
Best Local Similarity 63.9%; Pred. No. 2.4e-221;
Matches 523; Conservative 228; Mismatches 67; Indels 0; Gaps 0;
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DB 17 GAUCCAGAGUAGGGGUGUUAUUCUUGGUGGUGUCCAGUUCAGAAACAGAAAC 76
QY 424 CCTGTTCCGACTACTGTCTCTCCATATCGTCAATCTTCTCAGAGATTGGGAGCCCTGCG 483
DB 77 CCUGCCGGAUUAUUGCCUUCUACUUCUGGCGAGGAGGAGGAGCCUUG 136
QY 484 CGGAACATGAGAAACATCATCAGAGATTCTTGAAGCCCTGCTGTGTTACAGGCGGG 543
DB 137 ACGAUCAGGAGAAACUACUACAGAGAUUCCUAGAGCCUUCUUGUUAACAGGCGGG 196
QY 544 TTTTCTGTGTGAAGAATCTCAATACCGAGAGTCTAGCTCGGTGAGCTTCT 603
DB 197 UUUUUUUUUUUGAACAUAUCCUACAUAUCCGACAGUUAUCCGUGGAGUUAU 256
QY 604 CTCAATTTTCTAGGGGAACTACCGTGTCTTGGCAAAATTCGAGTCCCAACTCC 663
DB 257 CUCAUUAUUUUGAGGGGAGUACCCGUGUUCUUGGCAAAUUCGAGUCCCAACUCC 316
QY 664 AATCACTCACTCACTCTCTCTCTCACTTCTCTGTTATGCTGATGTGTGCGG 723
DB 317 AAUACACUCACCAACUCCUUGUCCUUAUUUUGUUAUCCGUGAGUUGUUGCGG 376
QY 724 CGTTTATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
DB 377 GCUUUUUUUUUAAGAGAAACUCCUGACGAAAGCUUGUUAUCCUUAUUUUUUUU 436
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DB 437 GAUUAUUAAGUAUUGUCCGCUUUGUUCUUAUUCGAGUUAUUAACAAACAGUA 496
QY 844 GAGCACTGAGAGCCTGCAAGCTCTGCTCAAGAACTCTATATCTCTCTCTCTG 903
DB 497 GGACCAUGCAAAACUCCGACGACUCCUUAAGGCAACUUAAGUUUCCUUAUG 556
QY 904 TGTACAAAACCTTGGATGGAACAGCACTGATTCATCCATCACTCCGAGCTTC 963
DB 557 UGUUACAAAACUACGAGUAGAAUUGACUUAUCCUUAUCCAGUCCUGGUGUUC 616
QY 964 GGAATAATCTATGGAAGTGGGCTCAGCCGTTTCTCTGAGTCAAGTTACAGTCA 1023
```

```
DB 617 GCAAAAUAACUAGGAGAGGAGCCUACUCCGUAUUUCUUGACUUAUUAAGUCCCA 676
QY 1024 TTGTTCAAGTGTGTGAGGGCTTCCGCCCATCTGTTGAGTTTACATATAGATGATG 1083
DB 677 UUUUUUUGAGUUGUUGAGGUGUUCUCCCAACUUGUUGUUGUUGUUGUUGUUG 736
QY 1084 TTGTACTGGGGGCGCAAGCTGTGACACATCTTGAATCCCTTTTACCGCTGTACCAAT 1143
DB 737 UGUUUAUUGGGGCGCAAGUUGUAGAGUUGUUGUUGUUGUUGUUGUUGUUGUUG 796
QY 1144 TTTCTTGTCTTGTGGTATACATTTAAACCTATATAA 1181
DB 797 UUUUUUUUUUUGUUGUUAUUAACCUUAACAAA 834
```

```
RESULT 4
US-10-383-317-15
; Sequence 15, Application US/1038317
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juha
; APPLICANT: Bass, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/10/383,317
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 15
; LENGTH: 849
; TYPE: DNA
; ORGANISM: Woodchuck hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(849)
; OTHER INFORMATION: Woodchuck hepatitis B virus (WH8) surface antigen
US-10-383-317-15
```

```
Query Match      34.9%; Score 412; DB 6; Length 849;
Best Local Similarity 71.6%; Pred. No. 5.9e-124;
Matches 557; Conservative 0; Mismatches 215; Indels 6; Gaps 1;
```

```
QY 393 TGTGTGAGCTTCAGTTACAGAAACAGTAACCTGTTCGACTACTGTCTCTCCATATC 452
DB 78 TGCCTATAGAGATCTTTTACACACTTAAGCCCTGCGGTCTCTATCTGATCACCATAT 137
QY 453 GTCAATCTTCTCAGAGATTGGGAGCCCTGCGGAAATGAGAAATCACAATCAGATT 512
DB 138 GTCTCTCCCTCGAGACTGGGAGCTGCACTGTACACGGAGATGTACCACTAAATCT 197
QY 513 CCTAGAACCCCTGCTGCTGTGTACAGCGGGGTTTTCTTGTGACAAAGATCTTCAAT 572
DB 198 CCTAGAGACTCTCGAGAGATTACAGTGTGATTTCTTGTGACAAAATCTTAACAT 257
QY 573 ACCGAGAGTGAAGCTGTGTGAGACTTCTCTCAATTTTCTAGGGGGAACCTACCTGTG 632
DB 258 AGCTAGAGATCTAGATTGTGTGTGATCTTCTCAGTTTCCAGGGGCGATACAGAGTG 317
QY 633 TCTTGGCCAAAATTTGCAAGTCCCAACCTCAATACACCAACCTCTGCTCCCAAC 692
DB 318 CACTGGCCAAAATTTGCAAGTCTCAACCTTGCAAAACCTTGCACCTCTGCTCAACAC 377
QY 693 TTGTCTGATTATCGCTGAGATGTCTCGGCGTTTATCAATCTTCTCTCATCTCTCT 752
```

```
Db      378 TTGCATAGGCTTGTGGATGATATCTGCGCGGTTTTATCATATACCTATTAGTCTGCT 437
Qy      753 GCTATGCGCTCATCTTCTTGTGGTCTTCTGACATATCAAGTATGTTGCGCGGTTGTC 812
Db      438 GCTGTGCTCATCTTCTTGTGGTCTTCTGACATATCAAGTATGTTGCGCGGTTGTC 497
Qy      813 TCTAATTCAGAGATCTTCAACCAACAGAGGAGCATGAGAGCTGACAGTCTCTGC 872
Db      498 TCTTCAACCAACCAACAGAGGAGCATGAGAGCTGACAGTCTCTGC 551
Qy      873 TCAAGAGACTCTATGATATCCCTCTGTGTGTGATACAAAACCTTGGATGGAATCTGCAC 932
Db      552 ACAAGACATGATATCTCTCTTATCTGTGTGTGTAAACCTTACGAGAGAAATTTGCAC 611
Qy      933 CTGTATATCCATCCCATCATCTCTGAGGCTTTCGAAAAATTCCTATGAGAGTGGGCTCAGC 992
Db      612 TTGTGTGCGCATCCCTTCATCATAGGCTTTAGAGAAATTCCTATGAGAGTGGGCTTACG 671
Qy      993 CCGTTTCTCTGCTGCTAGTTTACTAGTGCATTTGTTCACTGAGTTCGTAAGGCTTTTCCC 1052
Db      672 CCGTTTCTCTGCTGCTAGTTTACTAGTGCATTTGTTCACTGAGTTCGTAAGGATTTCCCT 731
Qy      1053 CACTGTTTGGCTTTCAGATATATGAGATGATGTTTACTGGGGGCGCAAGCTGTACACCAT 1112
Db      732 CATTTGCGGTGTTTGTCTTATATGAGATGATTTGGTTTGGGGGCGCGCACCTTTCAGACAT 791
Qy      1113 CTGAGTCCCTTCTTTCACGCTGTTTACCAATTTTCTTGTGTTGGGTATACATTTAA 1170
Db      792 CTTACCGCCATTTATTCCTCATATTTGTCTGTTTCTTGAATTTGGGTATACATTTGA 849
```

```
RESULT 5
PCT-US03-18993-1
; Sequence 1, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-1
```

```
Query Match      10.6%; Score 124.8; DB 1; Length 128;
Best Local Similarity 98.4%; Pred. No. 1.4e-30;
Matches 126; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      630 GTGTCTTGGCCAAATTCGAGTCCCAACCTCCATCATCAACCAACTCTGTCTCTCC 689
Db      1 GTGTCTTGGCCAAATTCGAGTCCCAACCTCCATCATCAACCAACTCTGTCTCTCC 60
Qy      690 AACTTGTCTGTTATGCTGGAGTGTGTGCGGCGTTTATCATCTTCTCTCATCTT 749
Db      61 AATTGTCTGTTATGCTGGAGTGTGTGCGGCGTTTATCATCTTCTCTCATCTT 120
Qy      750 GCTGCTAT 757
Db      121 GCTGCTAT 128
```

```
RESULT 6
PCT-US03-18993-68
; Sequence 68, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-68
```

```
Query Match      7.5%; Score 88.2; DB 1; Length 93;
Best Local Similarity 96.8%; Pred. No. 1.1e-18;
Matches 90; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      585 AGACTCGTGTGAGTCTCTCATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAA 644
Db      1 AGACTCGTGTGAGTCTCTCATTTTCTAGGGGGAATCACCGTGTGTCTTGGCCAAA 60
Qy      645 TTGCGAGTCCCCCACTTCATCATCTCACCAC 677
Db      61 TTGCGAGTCCCCCACTTCATCATCTCACCAC 93
```

```
RESULT 7
PCT-US03-18993-69
; Sequence 69, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-69
```

```
Query Match      6.0%; Score 71.4; DB 1; Length 73;
Best Local Similarity 98.6%; Pred. No. 2.9e-13;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      994 CGTTTCTCTGCTCAGTTCATCTAGTGCATTTTGTTCAGTGTCTGAGGCTTTCCCC 1053
Db      1 CGTTTCTCTGCTCAGTTCATCTAGTGCATTTTGTTCAGTGTCTGAGGCTTTCCCC 60
```

Qy	1054	ACTGTTTGCTTT	1066
Db	61	ACTGTTTGCTTT	73

```

RESULT 8
PCT-US03-18993-67/C
; Sequence 67, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; Title of Invention: Hepatitis B Virus
; FILE REFERENCE: GPL34-02.0T
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-67

```

```

RESULT 9
PCT-US03-18993-95/c
Sequence 95, Application PC/TUS0318993
GENERAL INFORMATION:
APPLICANT: Linnen, Jeffery M.
APPLICANT: Kolik, Daniel P.
APPLICANT: Dockter, Janel M.
APPLICANT: Getman, Dannon K.
APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Loy, Mary
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Hepatitis B Virus
FILE REFERENCE: GPR34-02.UT
CURRENT APPLICATION NUMBER: PCT/US03/18993
CURRENT FILING DATE: 2003-06-13
PRIORITY APPLICATION NUMBER: 60/389,393
PRIORITY FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 95
LENGTH: 59
TYPE: DNA
ORGANISM: Hepatitis B Virus
PCT-US03-18993-95
Query Match          4.9%; Score 57.4; DB 1; Length 59
Best Local Similarity 98.3%; Pred. No. 9.7e-09;

```

	Matches	56; Conservative	0; Mismatches	1; Indels	0; Gaps	0
Qy	736	TTCCCTTCATCCGCGTGGTATGCGCTCATCTCTGTTGGTTCCTTCGAGCATATCAAG	794			
Db	59	TTCCCTTCGATCCGCGCGTATGCGCTATCTCTGTTGGTTCCTTCGAGCATATCAAG	1			

```

RESULT 10
US-10-388-918A-7
; Sequence 7, Application US/10388918A
; GENERAL INFORMATION:
; APPLICANT: Browne, Kenneth A.
; TITLE OF INVENTION: Inversion Probes
; FILE REFERENCE: GPl30-03.CPl
; CURRENT APPLICATION NUMBER: US/10/388,918A
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/325,600
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 10/259,272
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ. ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO. 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
; US-10-388-918A-7

```

```

RESULT 11
PCT-US03-18993-4/C
Sequence 4, Application PC/TUS0318993
GENERAL INFORMATION:
APPLICANT: Linmen, Jeffery M.
APPLICANT: Kolk, Daniel P.
APPLICANT: Dockter, Janel M.
APPLICANT: Getman, Damon K.
APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Loy, Marcy
APPLICANT: Stringfellow, Leslie A.
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Hepatitis B Virus
FILE REFERENCE: GPI34-02.UT
CURRENT APPLICATION NUMBER: PCT/US03/18993
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/389,393
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 54
TYPE: DNA
ORGANISM: Hepatitis B Virus
PCT-US03-18993-4

```

RESULT 12

```
PCT-US03-18993-84
; Sequence 84, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-84
```

```
Query Match          4.2%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1004 GGCTCAGTTACTAGTGCATTTGTCAGTGGTCGAGGGCTTTCCCCC 1053
DB      1 GGCTCAGTTACTAGTGCATTTGTCAGTGGTCGAGGGCTTTCCCCC 50
```

```
RESULT 13
PCT-US03-18993-2
; Sequence 2, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-2
```

```
Query Match          4.1%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 7.8e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      708 CTGATGTCCTGGGCGTTTATCATCTTCCTTCATCTGCTGCTAT 757
DB      1 CTGATGTCCTGGGCGTTTATCATCATTCCTTCATCTGCTGCTAT 50
```

```
RESULT 14
PCT-US03-18993-78
; Sequence 78, Application PC/TUS0318993
; GENERAL INFORMATION:
```

```
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-78
```

```
Query Match          3.6%; Score 43; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      994 CGTTTCTCGCTCAGTTACTAGTGCATTTGTCAGTGGT 1036
DB      1 CGTTTCTCGCTCAGTTACTAGTGCATTTGTCAGTGGT 43
```

```
RESULT 15
PCT-US03-18993-142/c
; Sequence 142, Application PC/TUS0318993
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: PCT/US03/18993
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 142
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
PCT-US03-18993-142
```

```
Query Match          3.6%; Score 42.8; DB 1; Length 46;
Best Local Similarity 95.7%; Pred. No. 0.0005;
Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      768 CTTGTTGTTCTTCTGACATATCAAGTATGTCGCCGTTGCTT 813
DB      46 CTTATGTTCTTCTGATATATCAAGTATGTCGCCGTTGCTT 1
```

```
Search completed: September 15, 2003, 03:52:06
Job time : 289 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 00:34:55; Search time 3084 Seconds
(without alignments)
15666.105 Million cell updates/sec

Title: US-09-821-877-1

Perfect score: 1181

Sequence: 1 atggggcagaactcttcacc.....tacatttaaccctaataa 1181

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hcgo_hum:*

40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	95.9	2612	6 E00007	E00007 DNA coding
2	1133	95.9	2743	6 A08967	A08967 Hepatitis B
3	1133	95.9	2743	6 A08967	A08967 human hepat
4	1128.2	95.5	8007	6 BD1818	BD1818 Hepatitis B
5	1117.2	94.6	1201	6 AR011346	AR011346 Sequence
6	1117.2	94.6	1201	6 AR011346	AR011346 Sequence
7	1117.2	94.6	1285	6 AR011345	AR011345 Sequence
8	1117.2	94.6	1285	6 AR011345	AR011345 Sequence
9	1117.2	94.6	2342	6 A32618	A32618 Synthetic C
10	1115.6	94.5	1170	14 AB074844	AB074844 Hepatitis
11	1114	94.3	1170	14 HBAJ3116	AU003116 Hepatitis
12	1112.4	94.2	1170	14 AB074842	AB074842 Hepatitis
13	1110.6	94.0	1149	14 HBUS5226	HBUS5226 Hepatitis B
14	1107.4	93.8	1149	14 HBUS5225	HBUS5225 Hepatitis B
15	1107.4	93.8	1401	14 HBVPS125P	X77310 Hepatitis B
16	1105.8	93.6	1149	14 HBUS5223	HBUS5223 Hepatitis B
17	1102.8	93.4	1170	14 AB074843	AB074843 Hepatitis
18	1102.6	93.4	1149	14 HBUS5224	HBUS5224 Hepatitis
19	1099.4	93.1	1149	14 HBUS5227	HBUS5227 Hepatitis
20	1096.2	92.8	1149	14 HBUS5228	HBUS5228 Hepatitis
21	1088.2	92.1	2348	6 AR097815	AR097815 Sequence
22	1079.6	91.4	1171	14 HBVPS125A	X77309 Hepatitis B
23	1079.4	91.4	3995	14 HSHBV	X72213 H. sapiens G
24	1057.2	89.5	1171	14 HBVPS125M	X77308 Hepatitis B
25	1054.6	89.3	1570	14 AY221115	AY221115 Hepatitis
26	1049.2	88.8	1158	14 HBVSF3	AU003027 Hepatitis
27	1048.4	88.8	1170	14 AF388668	AF388668 Hepatitis
28	1044	88.4	1164	14 HBVSF4	AU003028 Hepatitis
29	1043.4	88.3	3182	14 HEPVCG	D00220 Hepatitis B
30	1039.8	88.0	1342	14 AB033273	AB033273 Hepatitis
31	1039.8	88.0	1342	14 AB033273	AB033273 Hepatitis
32	1038.2	87.9	1342	14 AB033272	AB033272 Hepatitis
33	1037.8	87.9	1164	14 AF391286	AF391286 Hepatitis
34	1034.6	87.6	1164	14 HBVSF2	AU003026 Hepatitis
35	1034	87.6	1342	14 AB033275	AB033275 Hepatitis
36	1028.8	87.1	1200	14 AB074845	AB074845 Hepatitis
37	1025.8	86.9	3182	14 HBV131567	A1131567 Hepatitis
38	1022.6	86.6	1436	14 AY040800	AY040800 Hepatitis
39	1021	86.5	1436	14 AY040798	AY040798 Hepatitis
40	1020.6	86.4	3248	6 AX151112	AX151112 Sequence
41	1019.4	86.3	3068	14 AF233236	AF233236 Hepatitis
42	1019.4	86.0	1436	14 AY040801	AY040801 Hepatitis
43	1016.2	86.0	1436	14 AY040803	AY040803 Hepatitis
44	1013	85.8	1436	14 AY040804	AY040804 Hepatitis
45	1013	85.8	1436	14 AY040804	AY040804 Hepatitis

ALIGNMENTS

RESULT 1

E00007

LOCUS E00007 2612 bp DNA linear PAT 29-SEP-1997

DEFINITION E00007 DNA coding of HBV antigen.

ACCESSION E00007.1 GI:2166318

VERSION E00007.1

KEYWORDS JP 1980104887-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2612)

AUTHORS Kanesu,M. and Hainteu,E.S.

TITLE REARRANGED DNA MOLECULE AND METHOD

JOURNAL Patent: JP 1980104887-A 1 11-AUG-1980;

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COMMENT
BIOMEN NV
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PN JP 1980104887-A/1
PD 11-AUG-1980
PR 20-DEC-1979 JP 1979164945
PR 22-DEC-1978 GB 78 49907, 27-DEC-1978 GB 78 50039, PR
01-NOV-1979 GB 79 7937910
PI KENESU MARIE, HAINTSU ERUNSUTO SHIYARPA
PC C12N15/00, C07H21/04, C12N1/00, C12P19/34, C12P21/02, C12Q1/00, PC
C12Q1/70//
PC C12R1/125, C12R1/19, C12R1/38, C12R1/645;
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CC hypothetical: No;
CC anti-sense: No;
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Best Local Similarity 97.5%; Pred. No. 0;
Matches 1151; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 ATGGGAGAGATCTTTCCACAGCAATCCCTGGGATTTCCCGACCAACAGTTGGAT 60
DB 1035 ATGGGAGAGATCTTTCCACAGCAATCCCTGGGATTTCCCGACCAACAGTTGGAT 1094
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DB 1635 TCTCTCAATTTCTAGGGGAACTACCGGTGTGTCTTGGCCAAATTTGCAAGTCCCAACC 1694
QY 661 TCCAAATCACTACCAACCTCTGCTCCCAACTGTCTGTATGTGCTGAGAGTGTCTG 720
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LOCUS Hepatitis B virus genes for core antigen and surface antigen.
DEFINITION A08967
ACCESSION A08967
VERSION A08967.1 GI:411872
KEYWORDS
SOURCE
ORGANISM
Hepatitis B virus
Hepatitis B virus
Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
1 (bases 1 to 2743)
AUTHORS Murray, K. and Schaller, H. E.
TITLRE Recombinant DNA molecules and their method of production
JOURNAL Patent: EP 0374869-A 5 27-JUN-1990;
Biogen, Inc.; BIOGEN, INC
LOCATION/Qualifiers
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BASE COUNT 638 a 728 c 579 g 798 t

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Query Match 95.9%; Score 1133; DB 6; Length 2743;
 Best Local Similarity 97.5%; Pred. No. 0;
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QY 1 ATGGGCGAGAAATCTTTCACAGCAATCTCTGGAGATTCTTCCGACCAAGTTGAT 60
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 QY 61 CGAGCTTCAGAGCAAAACCAACAATCCAGATTGGAGTTCAATCCCAAGAGACAC 120
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 QY 121 TGGCCAGAGCGCAACAGGTAGAGCTGGAGATTCCGAGCTGGGGTTCCACCGAC 180
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 QY 181 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGGATTAACAACAACCTTGCAGCA 240
 DB 1215 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGGATTAACAACAACCTTGCAGCA 1274
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RESULT 3
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 LOCUS human hepatitis b virus subtype adyw antigen genes (core antigen
 DEFINITION and surface antigen).
 ACCESSION J02202
 VERSION J02202.1 GI:329637
 KEYWORDS
 ORGANISM
 HEPADYW
 Hepatitis B virus
 Hepatitis B virus
 Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 REFERENCE
 1 (bases 1 to 2743)
 Paeek,M., Goro,T., Gilbert,W., Zink,B., Schaller,H., Mackay,P.,
 Leadbetter,G. and Murray,K.
 Hepatitis B virus genes and their expression in E. coli
 JOURNAL Nature 282 (5739), 575-579 (1979)
 MEDLINE 81012115
 PUBMED 399329
 COMMENT
 Original source text: hbv subtype adyw from human.
 cf hbvayw and whnswg. hbvayw is hepatitis b core antigen protein,
 and hbvayw is surface antigen protein.
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Best Local Similarity 97.5%; Pred. No. 0;
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QY      121  TGGCCAGACCCCAACAAGTAGAGCTGAGACATTCCGACTGGGGTCCACCCGAC 180
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RESULT 4
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LOCUS      BD181818
DEFINITION Hepatitis B virus vectors for gene therapy.
ACCESSION  BD181818
VERSION     BD181818.1 GI:30792736
KEYWORDS   JP 2002320480-A/3.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 8007)
AUTHORS   Ryu,W., Jeong,J.K., Lee,J., Cho,W.Y. and Yoon,G.S.
TITLE     Hepatitis B virus vectors for gene therapy
JOURNAL   Patent: JP 2002320480-A 3 05-NOV-2002;
          WANG-SHICK RYU
COMMENT   OS Unidentified
          PN JP 2002320480-A/3
          PD 05-NOV-2002
          PF 20-APR-2001 JP 2001122392
          PR 20-APR-2000 KR 2000-21070,12-APR-2001 KR 2001-19645 PI
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          SOON YOON
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          structure ; bases 3212 - 3272 CC 5'- DR1 ; bases 7 - 17
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          CC Poly A signal ; bases 3281-3286
          CC 3'- DR2 ; bases 2955 - 2965
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          ORF ; bases 490 - 2985 (exclude stop codon) CC S2 ORF ; bases
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Best Local Similarity 97.2%; Pred. No. 0;
Matches 1148; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGGAGCAAACTCTTCCACGACATCTCTGGATTTCTTCCGACCAAGTTGAT 60
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DB 1991 TTGGGAAAATTCCTATGAGAGTGGGCTCAGCCGCTTCTCTGCTCAGTTACTAGTG 2050
QY 1021 CCATTTGTTAGTGTGTTGTTAGAGGCTTCCCACTGTTTGGCTTCAATATGATG 1080
DB 2051 CCATTTGTTAGTGTGTTGTTAGAGGCTTCCCACTGTTTGGCTTCAATATGATG 2110
QY 1081 ATGTTGTAATGGGAGCCAAAGTCTGACACCAATCTTGAATCCCTTTTACCCGTTACCA 1140
DB 2111 ATGTTGTAATGGGAGCCAAAGTCTGACACCAATCTTGAATCCCTTTTACCCGTTACCA 2170
QY 1141 ATTTTCTTTTGTCTTTGGTATACATTTTAACCTTAATAA 1181
DB 2171 ATTTTCTTTTGTCTTTGGTATACATTTTAACCTTAATAA 2211

RESULT 5
AR011346
LOCUS AR011346 1201 bp DNA linear PART 04-DEC-1998
DEFINITION Sequence 218 from patent US 5762938.
ACCESSION AR011346
VERSION AR011346.1 GI:3969336
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Paolietti,E., Pertus,M.E., Taylor,J., Tartaglia,J., Norton,E.K., Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E., Cox,W.I., Audomest,d.-C.,Francis, and Gettig,R.Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US(5762938-A)218 09-JUN-1998;
FEATURES Location/Qualifiers
source 1..1201
/organism="unknown"
BASE COUNT 265 a 350 c 255 g 331 t
ORIGIN

Query Match 94.6%; Score 1117.2; DB 6; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGGAGCAAACTCTTCCACGACATCTCTGGATTTCTTCCGACCAAGTTGAT 60
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QY 61 CCAAGCTTTCAGAGCAAAACCAACATTCAGATTGGGACTTCAATCCCAAGAGACACC 120
DB 92 CCAAGCTTTCAGAGCAAAACCAACATTCAGATTGGGACTTCAATCCCAAGAGACACC 151
QY 121 TGGCCAGACGCCAACAAAGGTAGAGCTGAGCATTCGAGCTGGGGTTCAACCCAGCCAC 180
DB 152 TGGCCAGACGCCAACAAAGGTAGAGCTGAGCATTCGAGCTGGGGTTCAACCCAGCCAC 211
QY 181 GAGAGCTTTTGGGGTGAGCCCTCAGGCTCAGGCGATACCAAAACCTTGGCCAGCAAT 240
DB 212 GAGAGCTTTTGGGGTGAGCCCTCAGGCTCAGGCGATACCAAAACCTTGGCCAGCAAT 271
QY 241 CGGCTCTCTGCTTCCACCAATGCGCATGAGAAAGGACCTTACCCGCTGTCTCAACT 300
DB 272 CGGCTCTCTGCTTCCACCAATGCGCATGAGAAAGGACCTTACCCGCTGTCTCAACT 331
QY 301 TTGAGAAACATCATCTCTCAAGCCATGAGTGAAGTCCACAACTTTCCACCAACTCTG 360
DB 332 TTGAGAAACATCATCTCTCAAGCCATGAGTGAAGTCCACAACTTTCCACCAACTCTG 391
QY 361 CAAGATCCCAAGAGTGAAGTGTATTTTCCCTGTGTGAGCTCCAGTTCAAGAAACAGTA 420
DB 392 CAAGATCCCAAGAGTGAAGTGTATTTTCCCTGTGTGAGCTCCAGTTCAAGAAACAGTA 451

QY 421 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTTCTGAGAGATTGGGACCT 480
DB 452 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTTCTGAGAGATTGGGACCT 511
QY 481 GCGGGAACATGGAGACATACATCAGAGATCTCTAGAGACCCCGTCGTGTTCACAGCG 540
DB 512 GCGGTAAACATGGAGACATACATCAGAGATCTCTAGAGACCCCGTCGTGTTCACAGCG 571
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DB 572 GGGTTCTCTTGTGTGACAGAGATCTCTCAATACCGAGAGTCTAGATCTGTGTGACT 631
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DB 632 TCTCTCAATTTTCTAGGGGGAATCAACGCTGTCTTGGCCAAATTTGCAAGTCCCAAC 691
QY 661 TCCAAATACATCCCAACCTCTCTGTCCTCAATCTGTCTGTGTATTCCTGTGTGTCTG 720
DB 692 TCCAAATACATCCCAACCTCTCTGTCCTCAATCTGTGTGTATTCCTGTGTGTCTG 751
QY 721 CGGCGTTTATCATCTCTCTCTCATCTGCTGCTAGCTCATCTTCTTGTGTCTT 780
DB 752 CGGCGTTTATCATCTCTCTCTCATCTGCTGCTAGCTCATCTTCTTGTGTCTT 811
QY 781 CTGAGACTATCAAGGATGTGCGCGTTTGTCTCTAAATTCAGAGATCTTCAACCAAGC 840
DB 812 CTGAGACTATCAAGGATGTGCGCGTTTGTCTCTAAATTCAGAGATCTTCAACCAAGC 871
QY 841 ACGGACCATGAGAGCTGACAGATCTCTGCTCAAGAACTCTATGTATCCCTCTCTGT 900
DB 872 ACGGACCATGAGAGCTGACAGATCTCTGCTCAAGAACTCTATGTATCCCTCTCTGT 931
QY 901 TGCTGTACAAACCTTGTGAGATGAAATGCACTGTATTCCTCATCTCATCTCTGGACT 960
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QY 961 TTGGGAAATTTCTATGAGAGTGGGCTCTCAGCCGTTTCTCTGAGTCAATTACTAGTG 1020
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QY 1141 ATTTTCTTTTGTCTTTGGGTATACATTTAA 1170
DB 1172 ATTTTCTTTTGTCTTTGGGTATACATTTAA 1201

RESULT 6
11784 LOCUS 1201 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 218 from patent US 5494807.
ACCESSION 117984
VERSION 117984.1 GI:1598339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Paolucci,E., Perkins,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audommet,J.-C.F. and Gettig,R.R.
TITLE NVNAC vaccinia virus recombinants comprising heterologous inserts
JOURNAL Patent: US 5494807-A 218 27-FEB-1996;
FEATURES location/Qualifiers
source 1..1201
/organism="unknown"

BASE COUNT 265 a 350 c 255 g 331 t
ORIGIN
Query Match 94.6%; Score 1117.2; DB 6; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGGGGGAGAAATCTTTCACACAGCAATCTCTGGGATTTCTTCCGACCAACAGTTGGAT 60
DB 32 ATGGGGGAGAAATCTTTCACACAGCAATCTCTGGGATTTCTTCCGACCAACAGTTGGAT 91
QY 61 CCAAGCTTCAGACCAACCAACCAATCCAGATTGGGACTTCAATCCCAACAGGACCC 120
DB 92 CCAAGCTTCAGACCAACCAACCAATCCAGATTGGGACTTCAATCCCAACAGGACCC 151
QY 121 TGAGCAGACGCCAACAAGTAGAGCTGAGCAATTCGSACTGAGGGTTTCAACCCAGCGAC 180
DB 152 TGAGCAGACGCCAACAAGTAGAGCTGAGCAATTCGSACTGAGGGTTTCAACCCAGCGAC 211
QY 181 GAGAGCCTTTTGGGGTGAAGCCTTCAGGCTCAGGGCAATACACAAACCTTGCAGCAAT 240
DB 212 GAGAGCCTTTTGGGGTGAAGCCTTCAGGCTCAGGGCAATACACAAACCTTGCAGCAAT 271
QY 241 CGGCTTCCTGCTTCACCAATGGCCAGTCAAGAAAGGCAAGCCCGCTGTCTCAACT 300
DB 272 CGGCTTCCTGCTTCACCAATGGCCAGTCAAGAAAGGCAAGCCCGCTGTCTCAACT 331
QY 301 TTGAGAAACATCATCTATCTCAAGCAGATGAGCAATCCCAACTTTCACCAACTCTG 360
DB 332 TTGAGAAACATCATCTATCTCAAGCAGATGAGCAATCCCAACTTTCACCAACTCTG 391
QY 361 CAAGATCCAGAGTGAAGGCTGTATTTCTCTGCTGTGTGTCTTCAAGTCAAGACAGTA 420
DB 392 CAAGATCCAGAGTGAAGGCTGTATTTCTCTGCTGTGTGTCTTCAAGTCAAGACAGTA 451
QY 421 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTTCTGAGAGATTGGGACCT 480
DB 452 AACCTGTTCGACTACTGTCTCTCCATATGTCATCTTTCTGAGAGATTGGGACCT 511
QY 481 GCGGGAACATGGAGACATACATCAGAGATCTCTAGAGACCCCGTCGTGTTCACAGCG 540
DB 512 GCGGTAAACATGGAGACATACATCAGAGATCTCTAGAGACCCCGTCGTGTTCACAGCG 571
QY 541 GGGTTTTCTTGTGTGACAGAGATCTCTCAATACCGAGAGTCTAGATCTGTGTGACT 600
DB 572 GGGTTCTCTTGTGTGACAGAGATCTCTCAATACCGAGAGTCTAGATCTGTGTGACT 631
QY 601 TCTCTCAATTTTCTAGGGGGAATCAACGCTGTCTTGGCCAAATTTGCAAGTCCCAAC 660
DB 632 TCTCTCAATTTTCTAGGGGGAATCAACGCTGTCTTGGCCAAATTTGCAAGTCCCAAC 691
QY 661 TCCAAATACATCCCAACCTCTCTGTCCTCAATCTGTGTGTATTCCTGTGTGTCTG 720
DB 692 TCCAAATACATCCCAACCTCTCTGTCCTCAATCTGTGTGTATTCCTGTGTGTCTG 751
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DB 812 CTGAGACTATCAAGGATGTGCGCGTTTGTCTCTAAATTCAGAGATCTTCAACCAAGC 871
QY 841 ACGGACCATGAGAGCTGACAGATCTCTGCTCAAGAACTCTATGTATCCCTCTCTGT 900
DB 872 ACGGACCATGAGAGCTGACAGATCTCTGCTCAAGAACTCTATGTATCCCTCTCTGT 931
QY 901 TGCTGTACAAACCTTGTGAGATGAAATGCACTGTATTCCTCATCTCATCTCTGGACT 960
DB 932 TGCTGTACAAACCTTGTGAGATGAAATGCACTGTATTCCTCATCTCATCTCTGGACT 991
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Db 992 TTGGAAAAATTCCTATGGAGTGGGCGTTCAGCCCGTTTCTCTGCTAGCTTACTAGTG 1051
 Qy 1021 CCATTGTTCACTGAGTTCGTAGAGGCTTTCCCACTGTTGGCTTTCAGTTATATGATG 1080
 Db 1032 CCATTGTTCACTGAGTTCGTAGAGGCTTTCCCACTGTTGGCTTTCAGTTATATGATG 1111
 Qy 1081 ATGTGTATGGGGGCGCAAGTCTGTACACCAATCTTGAGTCCCTTTTACCGCTGTTACCA 1140
 Db 1112 ATGTGTATGGGGGCGCAAGTCTGTACACCAATCTTGAGTCCCTTTTACCGCTGTTACCA 1171
 Qy 1141 ATTTCTTTTGTCTTGGGTATACATTTAA 1170
 Db 1172 ATTTCTTTTGTCTTGGGTATACATTTAA 1201

RESULT 7

LOCUS AR011345 1285 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 215 from patent US 5762938.
 ACCESSION AR011345
 VERSION AR011345.1 GI:3969335
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1285)
 Paolietti,E., Perkins,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
 Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
 Cox,W.I., Audemnet,J.-C., Francis, and Gettlig,R.Robert.
 Modified recombinant vaccinia virus and expression vectors thereof
 Patent: US 5762938-A 215 09-JUN-1998;
 Location/Qualifiers

FEATURES

source 1..1285
 /organism="unknown"
 BASE COUNT 284 a 364 c 272 g 365 t
 ORIGIN

Query Match 94.6%; Score 1117.2; DB 6; Length 1285;
 Best Local Similarity 97.2%; Pred. No. 0;

Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGGGCGAGAAATCTTTCCACAGCAATCTCTGGAGTTCTTCCGACCAAGTTGAT 60
 Db 116 ATGGGCGAGAAATCTTTCCACAGCAATCTCTGGAGTTCTTCCGACCAAGTTGAT 175
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 Db 176 CCAGCTTTAGAGCAAAACCAACAATCCAGATTGGGACTTCAATCCCAAGACACAC 235
 Qy 121 TGGCCAGAGCGCAACAAAGGTAGAGCTGAGCAATTCGAGCTGGGGTTTACCCCAACGCGAC 180
 Db 236 TGGCCAGAGCGCAACAAAGGTAGAGCTGAGCAATTCGAGCTGGGGTTTACCCCAACGCGAC 295
 Qy 181 GGAGGCGTTTGGGGGTAGAGCCCTCAGGCTCAGGGGCATTAACAACAACTTGCAGCAAT 240
 Db 296 GGAGGCGTTTGGGGGTAGAGCCCTCAGGCTCAGGGGCATTAACAACAACTTGCAGCAAT 355
 Qy 241 CCGCTCTCTGCTTCCACCAATGCGCAGTCAAGAGGACCTTACCCCGCTGTCTCAACT 300
 Db 356 CCGCTCTCTGCTTCCACCAATGCGCAGTCAAGAGGACCTTACCCCGCTGTCTCAACT 415
 Qy 301 TTGAGAAACACTCATCTCTCAGCAAGTCAAGTGAATCTGCACAACCTTCCACCAAACTCTG 360
 Db 416 TTGAGAAACACTCATCTCTCAGCAAGTCAAGTGAATCTGCACAACCTTCCACCAAACTCTG 475
 Qy 361 CAAGATCCAGAGTGAAGAGTCTGTATTTCCCTGCTGTGGCTCCAGTTCAAGAACAGTA 420
 Db 476 CAAGATCCAGAGTGAAGAGTCTGTATTTCCCTGCTGTGGCTCCAGTTCAAGAACAGTA 535
 Qy 421 AACCTGTTCGAGTACTGTCTCTCCCAATGTCAATCTTTCGAGAGATTGGGACCT 480
 Db 536 AACCTGTTCGAGTACTGTCTCTCCCAATGTCAATCTTTCGAGAGATTGGGACCT 595

Qy 481 GCGCGAAACATGAGAGAACATCATCAGAGATTCTAGAACCCCTGCTGCTTACAGCGG 540
 Db 596 GCGTGAACATGAGAGAACATCATCAGAGATTCTAGAACCCCTGCTGCTTACAGCGG 655
 Qy 541 GGGTTTTCTTGTGACAAAGAAATCTCTACAAATCCGCAAGTCTGACTCTGGTGGACT 600
 Db 656 GGGTTTTCTTGTGACAAAGAAATCTCTACAAATCCGCAAGTCTGACTCTGGTGGACT 715
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 Db 716 TCTCAATTTCTAGGGGGAACTACCGTGTCTTGGCAAAATTCGACATCCCAAC 775
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 Db 836 CCGCGTTTATCATCTTCTCTTCAATCTGCTGCTATGCTCATCTTCTTGGTTCTT 895
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 Db 956 ACGGACCATGACGAGCGCTGACGACTCTCTGCTCAAGAACTCTATGATCCCTCTGT 1015
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 Qy 961 TTGGAAAAATTCCTATGGAGTGGGCGCTCAGCGGTTTCTCTGCTCAGTTACTAGTG 1020
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 Qy 1021 CCATTGTTCACTGAGTTCGTAGAGGCTTTCCCACTGTTGGCTTTCAGTTATATGATG 1080
 Db 1136 CCATTGTTCACTGAGTTCGTAGAGGCTTTCCCACTGTTGGCTTTCAGTTATATGATG 1195
 Qy 1081 ATGTGTATGGGGGCGCAAGTCTGTACACCAATCTTGAGTCCCTTTTACCGCTGTTACCA 1140
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 Qy 1141 ATTTCTTTTGTCTTGGGTATACATTTAA 1170
 Db 1256 ATTTCTTTTGTCTTGGGTATACATTTAA 1285

RESULT 8

LOCUS 117983 1285 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 215 from patent US 5494807.
 ACCESSION 117983
 VERSION 117983.1 GI:1598338
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1285)
 Paolietti,E., Perkins,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
 Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
 Cox,W.I., Audemnet,J.-C., F. and Gettlig,R.R.
 NYVAC vaccinia virus recombinants comprising heterologous inserts
 Patent: US 5494807-A 215 27-FEB-1996;
 Location/Qualifiers

FEATURES

source 1..1285
 /organism="unknown"
 BASE COUNT 284 a 364 c 272 g 365 t
 ORIGIN

Query Match 94.6%; Score 1117.2; DB 6; Length 1285;
 Best Local Similarity 97.2%; Pred. No. 0;

Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;				
Qy	1	ATGGGGGAGAAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCCGACCAACAGTTGGAT	60	
Db	116	ATGGGGGAGAAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCCGACCAACAGTTGGAT	175	
Qy	61	CCAGCTTTCAGAGCAACACCAACATTCAGATTGGGACTTTCAATCCCAACAGACACC	120	
Db	176	CCAGCTTTCAGAGCAACACCAACATTCAGATTGGGACTTTCAATCCCAACAGACACC	235	
Qy	121	TTGGCACAACGCGCAACAGGTAGAGGTGAGGATTCGAGCTGGGGTTACCCGACCGGAC	180	
Db	236	TGGCACAACGCGCAACAGGTAGAGGTGAGGATTCGAGCTGGGGTTACCCGACCGGAC	295	
Qy	181	GAGAGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATACAAACCTTTCAGCAAAAT	240	
Db	296	GAGAGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATACAAACCTTTCAGCAAAAT	355	
Qy	241	CCGCTCTCTGCTTCCACCAATCGCCAGTCAGAAAGGACGCTTACCCGCTGTCTCACT	300	
Db	356	CCGCTCTCTGCTTCCACCAATCGCCAGTCAGAAAGGACGCTTACCCGCTGTCTCACT	415	
Qy	301	TTGGAAACACTCATCTCCCAAGCCATGAGTGAACCTCCCACTTTCACCAAACTCTG	360	
Db	416	TTGGAAACACTCATCTCCCAAGCCATGAGTGAACCTCCCACTTTCACCAAACTCTG	475	
Qy	361	CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGGTGGCTCAGTTCAAGAACTGA	420	
Db	476	CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGGTGGCTCAGTTCAAGAACTGA	535	
Qy	421	AACCTGTTCCGACTACTGTCTTCCCATTCGTCATCTTCTGAGAGATTGGGACCT	480	
Db	536	AACCTGTTCCGACTACTGTCTTCCCATTCGTCATCTTCTGAGAGATTGGGACCT	595	
Qy	481	GGCGGGAACATNGAGAACATCAATCAGGATTCCTAGGACCCCGCTCGTGTACAGCG	540	
Db	596	GGCGGGAACATNGAGAACATCAATCAGGATTCCTAGGACCCCGCTCGTGTACAGCG	655	
Qy	541	GGGTTTTTCTTGTGACAAAGATCTTCACATACCGGAGAGTCTAGACTCGTGTGACT	600	
Db	656	GGGTTTTTCTTGTGACAAAGATCTTCACATACCGGAGAGTCTAGACTCGTGTGACT	715	
Qy	601	TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAAATTGGCAGTCCCAAC	660	
Db	716	TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAAATTGGCAGTCCCAAC	775	
Qy	661	TCCAAATCACTCAACAACTCTGTCTTCCCACTTCTCGGTAAATCGCTGGAATGTCTG	720	
Db	776	TCCAAATCACTCAACAACTCTGTCTTCCCACTTCTCGGTAAATCGCTGGAATGTCTG	835	
Qy	721	CGGCGTTTATCATCTTCTCTTCATCTCTGCTATGCTCATCTTCTTGTGTTCTT	780	
Db	836	CGGCGTTTATCATCTTCTCTTCATCTCTGCTATGCTCATCTTCTTGTGTTCTT	895	
Qy	781	CTGGAATATCAAGGATGTGCGGTTTGTCTCTAATTCAGAGATCTTCAACCAACAGC	840	
Db	896	CTGGAATATCAAGGATGTGCGGTTTGTCTCTAATTCAGAGATCTTCAACCAACAGC	955	
Qy	841	ACGGGACATGACAGAGCTGACAGATCTGTCTCAAGGAACTCTATGATTCCTCCCTG	900	
Db	956	ACGGGACATGACAGAGCTGACAGATCTGTCTCAAGGAACTCTATGATTCCTCCCTG	1015	
Qy	901	TGCTGTACAAACCTTCCGATGAAACCTGATATTCCTATTCCTATTCCTCGGCT	960	
Db	1016	TGCTGTACAAACCTTCCGATGAAACCTGATATTCCTATTCCTATTCCTCGGCT	1075	
Qy	961	TTTGGAAATTTCTATGGAGTGGGCTCAGCCGTTTCTCTGGCTCAGTTTACTAGTG	1020	
Db	1076	TTTGGAAATTTCTATGGAGTGGGCTCAGCCGTTTCTCTGGCTCAGTTTACTAGTG	1135	
Qy	1021	CCATTTGTTCAGTGGTGTGATGGGCTTCCCGCACTGTTAGCTTTCAGTTATATGATG	1080	
Db	1136	CCATTTGTTCAGTGGTGTGATGGGCTTCCCGCACTGTTAGCTTTCAGTTATATGATG	1195	

Qy	1081	ATGTTTACTGGGGGCCAAGTCTGTACACCATCTTAGTCCCTTTTACCCTGTTACCA	1140
Db	1196	ATGTGATATGGGGGCCAAGTCTGTACACCATCTTAGTCCCTTTTACCCTGTTACCA	1255
Qy	1141	ATTTTCTTTTGTCTTGGGATACATTAA	1170
Db	1256	ATTTTCTTTTGTCTTGGGATACATTAA	1285
RESULT 9			
A32618		2342 bp	DNA
LOCUS	A32618		linear
DEFINITION	Synthetic coding seq for pre-S1,pre-S2 and S hepatitis B antigen peptides.		
ACCESSION	A32618		
VERSION	A32618.1	GI:1567467	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 2342)		
AUTHORS	Thoma,H.A.D.		
TITLE	Peptide comprising hepatitis B surface antigen		
JOURNAL	Patent: EP 0304578-A 1 01-MAR-1989; Epitec Limited		
FEATURES			
Source	Location/Qualifiers		
BASE COUNT	493 a	661 c	524 g 664 t
ORIGIN	1..2342		
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Query Match	94.6%;	Score 1117.2;	DB 6; Length 2342;
Best Local Similarity	97.1%;	Pred. No. 0;	
Matches 1148;	Conservative 0;	Mismatches 33;	Indels 1; Gaps 1;
Qy	1	ATGGGGGAGAAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCCGACCAACAGTTGGAT	60
Db	12	ATGGGGGAGAAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCCGACCAACAGTTGGAT	71
Qy	61	CCAGCTTTCAGAGCAACACCAACATTCAGATTGGGACTTCAATCCCAACAGACACC	120
Db	72	CCAGCTTTCAGAGCAACACCGCAATTCAGATTGGGACTTCAATCCCAACAGACACC	131
Qy	121	TTGGCACAACGCGCAACAGGTAGAGGTGAGGATTCGGAATGGGAGTTCAATCCCAACAGACACC	180
Db	132	TTGGCACAACGCGCAACAGGTAGAGGTGAGGATTCGGAATGGGAGTTCAATCCCAACAGACACC	191
Qy	181	GAGAGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATACAAACCTTTCAGCAAAAT	240
Db	192	GAGAGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATACAAACCTTTCAGCAAAAT	251
Qy	241	CCGCTCTCTGCTTCCACCAATTCGCAATTCAGAAAGGAGCCCTTACCCGCTGTCTCAACT	300
Db	252	CCGCTCTCTGCTTCCACCAATTCGCAATTCAGAAAGGAGCCCTTACCCGCTGTCTCAACT	311
Qy	301	TTGGAAACACTCATCTCCCAAGCCATGAGTGAACCTCCACACTTTCACCAAACTCTG	360
Db	312	TTGGAAACACTCATCTCCCAAGCCATGAGTGAACCTCCACACTTTCACCAAACTCTG	371
Qy	361	CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGGTGGCTCAGTTGAGAACTGA	420
Db	372	CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGGTGGCTCAGTTGAGAACTGA	431
Qy	421	AACCTGTTCCGACTACTGTCTTCCCATATTCGTCATCTTCTGAGAGATTGGGACCT	480
Db	432	AACCTGTTCCGACTACTGTCTTCCCATATTCGTCATCTTCTGAGAGATTGGGACCT	491
Qy	481	GGCGGGAACATNGAGAACATCAATCAGGATTCCTAGGACCCCGCTCGTGTACAGCG	540
Db	492	GGCGGGAACATNGAGAACATCAATCAGGATTCCTAGGACCCCGCTCGTGTGTACAGCG	551

QY 541 GGGTTTCTGTTGACAAAGATCTCACAATACCCGAGTCTAGACTGTTGGTACT 600
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 QY 601 TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGACATCCCAACC 660
 DB 612 TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGACATCCCAACC 671
 QY 661 TCCAACTACTCACAACCTCTGCTCTCAACTGTCCTGTTATGCTGAGATGTCG 720
 DB 672 TCCAACTACTCACAACCTCTGCTCTCAACTGTCCTGTTATGCTGAGATGTCG 731
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 QY 841 AGGGGACATGACAGACCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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 DB 972 TTGCGAAAATTCCTATGAGAGTGGGCTGACGCCGTTTCTCTGCTGCTGCTGCT 1031
 QY 1021 CCATTTGCTCACTGCTTCTGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1032 CCATTTGCTCACTGCTTCTGAGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
 QY 1081 ATGTTGACTGGGGGCAAGTCTG-TACACATCTTGAAGTCCCTTTTACCGCTGTACC 1139
 DB 1092 ATGTTGACTGGGGGCAAGTCTG-TACACATCTTGAAGTCCCTTTTACCGCTGTACC 1151
 QY 1140 AATTTTCTTGTCTTGGGTATACATTTAAACCTTAATAAA 1181
 DB 1152 AATTTTCTTGTCTTGGGTATACATTTAAACCTTAATAAA 1193
 RESULT 10
 AB074844 1170 bp DNA linear VRL 28-MAY-2002
 LOCUS Hepatitis B virus gene for large s protein, complete cds,
 DEFINITION clone:BN648.
 ACCESSION AB074844
 VERSION AB074844.1 GI:21218033
 KEYWORDS
 SOURCE Hepatitis B virus
 ORGANISM Hepatitis B virus
 Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 REFERENCE
 1 Kato, H., Orito, E., Suganuchi, F., Ueda, R., Koshizaka, T., Yanaka, S.,
 Gish, R. G., and Mizokami, M.
 New hepatitis B virus genotyping system that allows for
 identification of mixed genotype infection
 Unpublished
 2 (bases 1 to 1170)
 JOURNAL Direct Submission
 AUTHORS Hideaki, K.
 TITLE Submitted (25-NOV-2001) Kato Hideaki, Nagoya City University,
 Second Department of Medicine; Kawasumi I, Mizuno-cho, mizuho-ku,
 Nagoya, Aichi 467-0001, Japan (E-mail:hideaki@nagoya2.jrc.or.jp,
 Tel:81-52-853-8216)
 FEATURES
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 1. 1170
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 BASE COUNT 249 a 345 c 254 g 322 t
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 Query Match 94.5%; Score 1115.6; DB 14; Length 1170;
 Best Local Similarity 97.1%; Pred. No. 0;
 Matches 1136; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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 DB 121 TGGCCAGACGCCAAGAAGTAGAGCTGGAGATTCGAGCTGGGGTTCAACCCACGAC 180
 QY 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGSCATTAACAACCTTGCAGCAAT 240
 DB 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGSCATTAACAACCTTGCAGCAAT 240
 QY 241 CGGCTCTGCTTCCACCAATGCGCATGCAAGAGGACCTTACCCGCTGTCTCACT 300
 DB 241 CGGCTCTGCTTCCACCAATGCGCATGCAAGAGGACCTTACCCGCTGTCTCACT 300
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 DB 361 CAAGATCCCAAGTAGAGGCTGTATTTCCCTGCTGTGCTCCAGTTACAGAACAGTA 420
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 DB 661 TCCAACTACTCACAACCTCTGCTCTCAACTGTCCTGTTATGCTGAGATGTCG 720
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Db	961	TTCCGAAAAATTCCTATGGGAGTGGGCCCCAGCCCGTTTCTCGTGCCTAGTTTACTAGT	1020
QY	1021	CCATTGTTCAGTGGTTCGTAGAGGCTTTCCCACTGTTGGCTTCAGTTATATGATG	1080
Db	1021	CCATTGTTCAGTGGTTCGTAGAGGCTTTCCCACTGTTGGCTTCAGTTATATGATG	1080
QY	1081	ATGTTGTAATGGGGCCCAAGTCTGTACACATCTTGAATCCCTTTTACCGCTGTACCA	1140
Db	1081	ATGTTGTAATGGGGCCCAAGTCTGTACACATCTTGAATCCCTTTTACCGCTGTACCA	1140
QY	1141	ATTTCTTTTGTCTTTGGGTATACATTAA	1170
Db	1141	ATTTCTTTTGTCTTTGGGTATACATTAA	1170
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LOCUS	AB074842	1170 bp DNA linear	VR1.28-MAY-2002
DEFINITION	Hepatitis B virus gene for large S protein, complete cde.		
ACCESSION	AB074842		
VERSION	AB074842.1	GI:21218029	
KEYWORDS	Hepatitis B virus		
SOURCE	Hepatitis B virus		
ORGANISM	Hepatitis B virus		
REFERENCE	1 Kato, H., Orito, E., Suganuchi, F., Ueda, R., Koshizaka, T., Yanaka, S.,		
AUTHORS	Glegh, R.G. and Mizokami, M.		
TITLE	New hepatitis B virus genotyping system that allows for		
JOURNAL	identification of mixed genotype infection		
REFERENCE	2 (bases 1 to 1170)		
AUTHORS	Hideaki, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-NOV-2001) Kato Hideaki, Nagoya City University,		
REFERENCE	Second Department of Medicine, Kawasumi 1, Mizuno-cho, mizuho-ku,		
AUTHORS	Nagoya, Aichi 467-0001, Japan (E-mail: hideaki@nagoya2.jrc.or.jp,		
TITLE	Tel:81-52-853-8216)		
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BASE COUNT	247 a 349 c 255 g 319 t		
ORIGIN			
Query Match	94.2% Score 1112.4; DB 14; Length 1170;		
Bert Local Similarity	96.9% Pred. No. 0;		
Matches 1134; Conservative	0; Mismatches 36; Indels 0; Gaps 0;		
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QY	61	CCAGCCTTCAGAGCAACCAACATTCAGATTGGACTTCATCCCAACAGACACC	120
Db	61	CCAGCCTTCAGAGCAACCAACATTCAGATTGGACTTCATCCCAACAGACACC	120

Db	61	CCAGCTTCAAGACAAACCGCAAAATCCAGATTGGGACTTCAATCCCAACAAAGAACCC	120
Qy	121	TGGCCAAACGCCCAACAAAGTTAGAGCTGAGACATTTGGACTGGGGTTCACTCCACCGCAC	180
Db	121	TGGCCAAACGCCCAACAAAGTTAGAGCTGAGACATTTGGACTGGGGTTCACTCCACCGCAC	180
Qy	181	GGAGGCGCTTTTGGGGGTGAGAGCCCTCAGGCTTCAGGGGCTTAAACAACACTTGGCAGCAAT	240
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Qy	301	TTGAGAAACACTCATCCTCAAGCCATCGATGSAATCTCACCAACTTTCCACCAACTCTG	360
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Qy	361	CAAAATCCGAGAGTGAAGTCTGTATTTCCGCTGCTGAGTGCCTCACTTACGAGAACGTA	420
Db	361	CAAAATCCGAGAGTGAAGTCTGTATTTCCGCTGCTGAGTGCCTCACTTACGAGAACGTA	420
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Qy	481	GCGGGAAACATGAGAAACATCAATCAGAGATTCTTGAAGACCCCTGCTCTGTATACAGCG	540
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Qy	541	GGGTTTTTCTGTGTGAACAAGATTCCTCAATACCGGAGTCTAAGTCTGTGTGACT	600
Db	541	GGGTTTTTCTGTGTGAACAAGATTCCTCAATACCGGAGTCTAAGTCTGTGTGACT	600
Qy	601	TCTCTCAATTTTTCAGGGGGGAACTACCGTGTGTTTGAGCCAAATTTGGCAGTCCCAAC	660
Db	601	TCTCTCAATTTTTCAGGGGGGAAACCAACCGTGTGTTTGAGCCAAATTTGGCAGTCCCAAC	660
Qy	661	TCCAACTACCTACCAACCTCTGTCTTCAACTTGTCTGTGTTATGCTGAGTGTCTG	720
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Qy	721	CGGCGTTTATCATCTTCTCTTATCTGTATCTGTGCTATGCTCATCTTCTTGTGGTCTT	780
Db	721	CGGCGTTTATCATCTTCTCTTATCTGTATCTGTGCTATGCTCATCTTCTTGTGGTCTT	780
Qy	781	CTGACATATCAAGGTATGTTGCCGCTTGTCTCTAATTCAGAGATCTTCAACACACAGC	840
Db	781	CTGACATATCAAGGTATGTTGCCGCTTGTCTCTAATTCAGAGATCTTCAACACACAGC	840
Qy	841	ACGGGACCAATGAGAGCTGCACAGACTCTGTCTCAAGAACTTATGATATCCTCTCGT	900
Db	841	ACGGGACCAATGAGAGCTGCACAGACTCTGTCTCAAGAACTTATGATATCCTCTCGT	900
Qy	901	TGCTGTACAAACCTTCGATGAGAACTGACCTGTATTCCTATCCATCATCTCTGGCT	960
Db	901	TGCTGTACAAACCTTCGCGACGGAATTTGACCTGTATTCCTATCCATCATCTTGGGCT	960
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Qy	1021	CCATTGTTCAGTGGTTCGTAGGGCTTTCGCCCACTTTTGAGCTTTCAGTTATATGATG	1080
Db	1021	CCATTGTTCAGTGGTTCGTAGGGCTTTCGCCCACTTTTGAGCTTTCAGTTATATGATG	1080
Qy	1081	ATGTTGTACTGGGGGCCAAGTCTGTACACCACTTGAATCCCTTTTACCGCTGTACCA	1140
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Qy	1141	ATTTTCTTTTGTCTTTGGGTATACATTTAA	1170
Db	1141	ATTTTCTTTTGTCTTTGGGTATACATTTAA	1170

RESULT 13
HBUS5226
LOCUS HBUS5226 1149 bp DNA linear VRL 15-FEB-1997
DEFINITION Hepatitis B virus large S protein (Pre-S/S) gene, partial cds.
ACCESSION U55226
VERSION U55226.1 GI:1518558
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 1149)
AUTHORS Moraes,M.T., Gomes,S.A. and Niel,C.
TITLE Sequence analysis of pre-S/S gene of hepatitis B virus strains of genotypes A, D, and F isolated in Brazil
JOURNAL Arch. Virol. 141 (9), 1767-1773 (1996)
MEDLINE 97049068
PubMed 8893798
REFERENCE 2 (bases 1 to 1149)
AUTHORS Niel,C.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1996) Christian Niel, Virology, Oswaldo Cruz Foundation, Av. Brasil, 4365, Rio de Janeiro, RJ 21045-900, Brazil
FEATURES
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QY 1141 ATTTTCTTT 1149
DB 1141 ATTTTCTTT 1149
RESULT 14
HBUS5225
LOCUS HBUS5225 1149 bp DNA linear VRL 15-FEB-1997
DEFINITION Hepatitis B virus large S protein (Pre-S/S) gene, partial cds.
ACCESSION U55225
VERSION U55225.1 GI:1518556
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 1149)
AUTHORS Moraes,M.T., Gomes,S.A. and Niel,C.

TITLE Sequence analysis of pre-S/S gene of hepatitis B virus strains of
JOURNAL genotypes A, D, and F isolated in Brazil
MEDLINE Arch. Virol. 141 (9), 1767-1773 (1996)
PUBMED 97049068
8893798
REFERENCE
AUTHORS 2 (bases 1 to 1149)
Niel, C.
JOURNAL Direct Submission
Submitted (17-APR-1996) Christian Niel, Virology, Oswaldo Cruz
Foundation, Av. Brasil, 4365, Rio de Janeiro, RJ 21045-900, Brazil

FEATURES
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1..1149
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BASE COUNT 239 a 350 c 250 g 310 t

ORIGIN

Query Match 93.8%; Score 1107.4; DB 14; Length 1149;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1123; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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DB 481 GCGTGAACATGAGAAATCAATCAGATTCTTAGAACCCCTTCTCGTTTACAGGCG 540
QY 541 GGGTTTTCTTGTGACAAAGATCCCAATACCGAGAGCTGAGCTGAGTGGACT 600
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QY 1141 ATTTTCTTT 1149
DB 1141 ATTTTCTTT 1149

RESULT 15
HBVPS12SP 1401 bp DNA linear VRL 01-FEB-1994
LOCUS
DEFINITION
Hepatitis B virus Pre S1, Pre S2 and S genes (patient P).
ACCESSION
X77310.1 GI:452615
VERSION
S gene; S protein; S1 gene; S1 protein; S2 gene; S2 protein;
surface protein.
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
1
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

REFERENCE
1
Lai, M.E., Mizoloni, A.P. and Balistreri, A.
Sequence analysis of HBV genomes isolated from patients with HBsAg
chronic liver disease
JOURNAL
Unpublished
2 (bases 1 to 1401)
Lai, M.E.
AUTHORS
Direct Submission
Submitted (19-JAN-1994) M.E. Lai, University of Cagliari, Institute
of Internal Medicine, Laboratory of Virology, Via San Giorgio 12,
09124 Cagliari, ITALY
JOURNAL
Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 00:33:45 ; Search time 290 Seconds
(without alignments)
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Title: US-09-821-877-1

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Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1131.4	95.8	2743	11	AA000003
3	1131.4	95.8	2743	11	AA004799
4	1128.2	95.5	8007	24	AA000003
5	1117.2	94.6	1201	13	AA029106
6	1117.2	94.6	1285	13	AA029104
7	1117.2	94.6	2342	10	AA093072
8	1020.6	86.4	3248	22	AAH77562

9	1020.6	86.4	3248	22	AA009091
10	1010.2	85.5	1203	22	AAH77564
11	1005	85.1	3835	11	AA005378
12	1001.8	84.8	4084	22	AA014316
13	1001.8	84.8	4496	22	AA014317
14	1000.6	84.7	1200	17	AA036611
15	1000.2	84.7	9325	20	AA223282
16	1000.2	84.7	9859	20	AA223286
17	997.6	84.5	2526	22	AA009101
18	995.6	84.3	1170	15	AA067970
19	992.8	84.1	1436	24	AB055200
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22	986	83.5	1167	12	AA010678
23	985.8	83.5	7463	20	AA223293
24	966	81.8	1161	12	AA010679
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29	946.6	80.2	1132	22	AAH7576
30	936.8	79.3	1107	22	AAH7580
31	933.4	79.0	1087	22	AAH7582
32	929.4	78.7	1090	22	AAH7581
33	923	78.2	1132	22	AAH7575
34	914.8	77.5	1079	22	AAH7578
35	914.8	77.5	1080	22	AAH7579
36	871.6	73.8	1066	22	AAH7583
37	817.2	69.2	3180	22	AAH42375
38	813.2	68.9	8717	24	AA016093
39	811.8	68.7	3220	21	AA288924
40	811.2	68.7	3182	24	AA031765
41	810.8	68.7	846	20	AA210968
42	808.8	68.5	1262	2	AA010005
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45	774.8	65.6	859	10	AA091823

ALIGNMENTS

RESULT 1
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ABV75781;
27-JAN-2003 (first entry)
Hepatitis B virus mutant envelope gene.
HBV; HBsAg; surface antigen; envelope; diagnosis; vaccine; gene;
mutant; ss.
Hepatitis b virus.
Key Location/Qualifiers
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/tag= a
/product= "HBsAg"
misc_feature 492..675
/tag= b
/note= "encodes mutant 'a' determinant; region also claimed in Claim 1"

WO200279217-A1.
10-OCT-2002.
26-MAR-2002; 2002WO-US09227.
30-MAR-2001; 2001US-0821877.

XX (ABBO) ABBOTT LAB.
 XX
 XX Coleman PF, Mushahwar IA;
 XX
 DR WPI; 2003-040642/03.
 DR P-PSDB; ABP5073.
 XX
 PT New nucleotide sequences, useful for detecting compounds that bind to
 PT SP41 protein or antibodies to the Hepatitis B virus surface antigen
 PT mutant or for creating primers and probes .
 XX
 PS Claim 1; Fig 1; 43bp; English.
 XX
 CC The present sequence is the nucleotide sequence of the entire
 CC envelope gene for a mutant hepatitis B virus (HBV) strain isolated
 CC from a French sample identified as 990525169. This is an HBV
 CC subtype ayw2, genotype D sequence which contains mutations leading
 CC to 3 amino acid substitutions in the encoded protein: Thr to Ala
 CC 123, which affects the H166 epitope; Trp to Leu 199, which is
 CC outside the 'a' determinant; and Ser to Thr 207, which is also
 CC outside the 'a' determinant. The present invention relates to the
 CC novel HBV mutant which has a modified 'a' determinant as a result
 CC of T123A amino acid substitution, and to methods of detecting this
 CC mutant, and/or antibodies to the mutant, in patient samples. The
 CC identification and detection of mutant HBV may lead to improved
 CC vaccine development and detection systems.
 CC
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 Query Match 100.0%; Score 1181; DB 25; Length 1181;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 661 TCCAAATCACTCAACAACCTCTCTCTCCAACTTGCTGCTGTTATGCTGAGATGTCTG 720
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 DB 721 CGGCGTTTATCATCTTCCCTTCATCTGCTGCTGATAGCTCATCTTCTTGGTGTCTT 780
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 DB 781 CTGAGATCAAGATATGTTGCCGTTTGTCTCTAATTCAGAGATCTCAACACACAGC 840
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 QY 901 TGCTGTACAAACCTTCGATGGAACCTGCACTGTAATCCATCCATCATCTGAGCT 960
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 DB 901 TGCTGTACAAACCTTCGATGGAACCTGCACTGTAATCCATCCATCATCTGAGCT 960
 QY 961 TTGGAAATTTCTATGAGAGTGGGCTCAGCCGTTTCTCTGAGCTCACTTACTAGTG 1020
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 |||||
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 XX
 AC AAN00003;
 XX
 DT 25-MAR-2003 (updated)
 DT 14-OCT-1992 (first entry)
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 XX
 KM Hepatitis B virus; antigen; antibody; diagnosis; vaccine; ss.
 XX
 OS Hepatitis B virus.
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 FH Key
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 FT 88..639
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 FT /note= "reading frame 1"
 FT 1524..2204
 FT /*tag= c
 FT /product= AAP00042; surface Ag
 FT /note= "reading frame 3"
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 XX EPI3828-A.
 XX
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PF 21-DEC-1979; 79EP-0123526.
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XX 22-DEC-1978; 78GB-0049907.
PR 27-DEC-1978; 78GB-0050039.
PR 01-NOV-1979; 79GB-0037910.
XX
XX (BIOU ) BIOGEN INC.
XX
XX Murray K, Schaller HE;
XX
XX WPI, 1990-195067/26.
DR P-PSDB; AAR05634, AAR05635, AAR06613.
XX
XX Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
PT put in detection of infection and in vaccine prodn.
XX
XX PS Disclosure; Page 7; ?pp; English.
XX
XX CC Polypeptide fragments encoded by the DNA sequence are antigenic for
CC HBV and may be used as a vaccine or in detection. Peptides may be
CC cultured in a suitable bacterial host such as E.coli.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 2743 BP; 638 A; 728 C; 579 G; 797 T; 1 other;

Query Match 95.8%; Score 1131.4; DB 11; Length 2743;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1150; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DB 1095 CGAGCTTCAGAGCAACCAACATCCAGATTGGGACTTCATCCGCAACAGAGACCC 1154
QY 121 TGGCCAGACGCCCAACAGTAGAGCTGAGCATTCGAGCTGGGGTTACCCGACCGCAC 180
DB 1155 TGGCCAGACGCCCAACAGTAGAGCTGAGCATTCGAGCTGGGGTTACCCGACCGCAC 1214
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DB 1215 GGAAGCCTTTTGGGGTGAAGCCTCAGGCTCAAGGCAATACAAACCTTGCCAGCAAT 1274
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DB 1455 AACCCTGTCCGATCTACTGTCTCCCATATCGCATATCTTCTGAGAGATTGGGAGACCT 1514
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DB 2115 ATGTTGTACTGGGGGCAACTCTGTACACATCTTATAGTCCCTTTTACCGCTTACCA 2174
QY 1141 ATTTCTTTTGTCTTTGGGATACATTTAAACCTTATAAA 1181
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RESULT 4
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ID AAS16092 standard; DNA; 8007 BP.
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XX
XX 14-FEB-2002 (first entry)
XX
XX HBV viral vector pCMV-HBV/30.
XX
XX HBV-ayw; alpha element; ss; chronic hepatitis B virus infection;
XX cis-acting element; viral vector; gene therapy; hepatitis C virus gene;
XX tumour suppressor; growth factor; hormone; cytokines; coagulation factor;
XX cellular ligand receptor; liver disease; genetic disease;
XX metabolic disease; haemophilia; cyclic; circular; pCMV-HBV/30.
XX
XX Hepatitis B virus.
OS Bacteriophage M13.
OS Escherichia coli.
OS Cauliflower mosaic virus.
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Qy      901 TGGTGTACAAACCTTGAGTGAAGTGAACCTGATGATCCATCCATCCTGGGCT 960
Db      1931 TGGTGTACCAACCTTGAGACGAAATTTGACCTGATGATCCATCCATCCTGGGCT 1990
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Qy      1021 CCATTGTCAGTGGTGGTGAAGGCTTCCGCCACTGTTGGCTTTCAGTTATATGAGATG 1080
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Qy      1081 ATGTTGACTGGGGGCCAAGTCTGTACACCATCTTGAAGTCCCTTTTACCGCTGTACCA 1140
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Qy      1141 ATTTCTTTTGTCTTTGGGCTATACATTAAACCTTAATAA 1181
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RESULT 5
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ID      AAQ29106 standard; DNA; 1201 BP.
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AC      AAQ29106;
XX
DT      25-MAR-2003 (updated)
DT      24-FEB-1993 (first entry)
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DE      13L promoter/S12/core gene.
XX
KM      Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
KM      vaccinia virus; Amara moorei entomopoxvirus; AmbPV; 42 kd; promoter;
KM      NYVAC; recombinant; HBV L; large pre-S antigen; lpsAg; fusion protein;
KM      pre-S region; S12/core; S1; S2; Copenhagen vaccine strain;
XX      vaccinia virus; virulence factor; deletion loci; recipient loci; ss.
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OS      Synthetic.
XX
FH      Key
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FT      /*tag= e
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PN      MO9215672-A1.
XX
PD      17-SEP-1992.
XX
PF      09-MAR-1992; 92WO-US01906.
XX
PR      07-MAR-1991; 91US-0666056.
PR      11-JUN-1991; 91US-0713967.
PR      06-MAR-1992; 92US-0847951.
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XX      (VIRO-) VIROGENETICS CORP.
PA
XX      Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP;
PI      Limbach KJ, Norton EK, Paolletti E, Perkins ME, Pincus SE;
PI      Riviére M, Tarteagila J, Taylor J;
XX
DR      WPI; 1992-331718/40.
DR      P-PSDB; AAR27474.
XX
PT      Vaccine comprises recombinant, attenuated pox-virus - use for
PT      vaccinating against viral infections such as rabies, hepatitis B,
PT      HIV, HSV, EBV, CMV, mumps etc.
XX
PS      Disclosure; Fig 15; 456pp; English.
XX
CC      The sequence given encodes the hepatitis B virus (HBV) L protein
CC      (large pre-S antigen, lpsAg) which is precisely linked to the Amara
CC      moorei entomopoxvirus (AmbPV) 42 kd promoter. This sequence was used
CC      in the construction of a NYVAC recombinant expressing the HBV gene.
CC      Other HBV genes were also used in the construction. These were HBV M
CC      protein (small pre-S antigen, spsAg) and a fusion protein composed of
CC      the entire pre-S region (S12/core, S1 + S2). Each of these gene
CC      sequences were inserted individually into three different sites of
CC      NYVAC separated by from each other by large regions of vaccinia DNA
CC      containing essential genes. NYVAC is a Copenhagen vaccine strain of
CC      vaccinia virus which has been modified by deletion of six non-essential
CC      regions of the genome encoding known or potential virulence factors.
CC      The deletion loci were engineered as recipient loci for the insertion
CC      of foreign genes. The spacing of the three inserted sequences ensured
CC      that any recombination that did occur would lead to disruption of the
CC      vaccinia genome and would cause unviable vaccinia virus. See also
CC      AAQ35501-864.
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 1201 BP; 265 A; 350 C; 255 G; 331 T; 0 other;

Query Match      94.6%; Score 1117.2; DB 13; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy      1 ATGGGCGAGAAATCTTTCACACAGCAATCTCTGGATTTCTTCCGACCAACGATTGGAT 60
Db      32 ATGGGCGAGAAATCTTTCACACAGCAATCTCTGGATTTCTTCCGACCAACGATTGGAT 91
Qy      61 CCAGCCTTGAGAGCAACCAACCAATCCAGATTGGAGCTTCAATCCCAACAGGACAC 120
Db      92 CCAGCCTTGAGAGCAACCAACCAATCCAGATTGGAGCTTCAATCCCAACAGGACAC 151
Qy      121 TGGCAGACGCCAACAAGTAGAGCTGAGCATTTGGAGTGGGTTTACCCGACCGCAC 180
Db      152 TGGCAGAGGCCAACAAGTAGAGCTGAGCATTTGGAGTGGGTTTACCCGACCGCAC 211
Qy      181 GAGGCGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACAACCTTGGCAAGAT 240
Db      212 GAGGCGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACAACCTTGGCAAGAT 271
Qy      241 CCGCTCTCGCTTCCACCAATGGCAGTCAAGGAGAGGAGCTCCCGCGCTGTCCACCT 300
Db      272 CCGCTCTCGCTTCCACCAATGGCAGTCAAGGAGAGGAGCTCCCGCGCTGTCCACCT 331
Qy      301 TTGAGAAACACTATCCTCAGAGCATGAGTGAAGTCCACAACTTTCCACCAACTCTG 360
Db      332 TTGAGAAACACTATCCTCAGAGCATGAGTGAAGTCCACAACTTTCCACCAACTCTG 391
Qy      361 CAAGATCCAGAGTGAAGGCTGTGATTTCTCTGTGTGGTGTCTCCAGTTAGAGAACGTA 420
Db      392 CAAGATCCAGAGTGAAGGCTGTGATTTCTCTGTGTGGTGTCTCCAGTTAGAGAACGTA 451
Qy      421 AACCGTTCCGACTCTGCTCTCCCATATGTCATATCTTCGAGGATTTGGGAGCCCT 480
Db      452 AACCGTTCCGACTCTGCTCTCCCATATGTCATATCTTCGAGGATTTGGGAGCCCT 511
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OY	481	GGCGGGAACATGAGAAACATCAATCAGAGATTCTTAGAGACCCTGCTGCTGTATACAGGG	540
Db	512	GGCGTGAACATGAGAAACATCAATCAGAGATTCTTAGAGACCCTTTCGGTTTACAGGG	571
OY	541	GGGTTTTCTGTGACAAGAATCCTCACAAATACCGCAGAGTCTAGACTCGTGTGAGCT	600
Db	572	GGGTTCTTCTGTGTACAAGAATCCTCACAAATACCGCAGAGTCTAGACTCGTGTGAGCT	631
OY	601	TCTCTCAATTTCTAGGGGGGAATCTACCGGTGTCTTTGGCAAAATTCGAGTCCCAAC	660
Db	632	TCTCTCAATTTCTAGGGGGGAATCTACCGGTGTCTTTGGCAAAATTCGAGTCCCAAC	691
OY	661	TCCAACTACTCAACCACTCTGTCTCTCCCACTTGTCTGTATTCGCTGAGTGTGTCTG	720
Db	692	TCCAACTACTCAACCACTCTGTCTCTCCCACTTGTCTGTATTCGCTGAGTGTGTCTG	751
OY	721	CGGCGTTTTATATCTTCTCTTCAATCTCTGTGCTATAGTCTCATCTTCTTGTGGTCTT	780
Db	752	CGGCGTTTTATATCTTCTCTCTTCAATCTCTGTGCTATAGTCTCATCTTCTTGTGGTCTT	811
OY	781	CTGACATCTCAAGGATATGTGGCCGTTTGTCTCTAATCCAGAGTCTTCAACCAAC	840
Db	812	CTGACATCTCAAGGATATGTGGCCGTTTGTCTCTAATCCAGAGTCTTCAACCAAC	871
OY	841	ACGGGACCATGCGAGCCTGCGAGACTCTGCTCAAGAACTCTATGTATCCTCTGT	900
Db	872	ACGGGACCATGCGAGCCTGCGAGACTCTGCTCAAGAACTCTATGTATCCTCTGT	931
OY	901	TGCTGTACAAAACCTTCCGATGGAACCTGCACTGTATTCGATCCATCTCGGGCT	960
Db	932	TGCTGTACAAAACCTTCCGATGGAACCTGCACTGTATTCGATCCATCTCGGGCT	991
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Db	992	TTCCGAAAATTTCTATGCGAGTGGGCTTCAGCCCGTTCCTCGGCTCAGTTTACTAGTG	1050
OY	1021	CCATTGTATCAGTGTGTGAGGGCTTCCCCACGTTTGGCTTTCAGTTATATGAGAG	1080
Db	1052	CCATTGTATCAGTGTGTGAGGGCTTCCCCACGTTTGGCTTTCAGTTATATGAGAG	1110
OY	1081	ATGTGTATCTGGGGGCCAAGTCTGTACACCATTTGAGTCCCTTTTACCGCTGTATACCA	1140
Db	1112	ATGTGTATCTGGGGGCCAAGTCTGTACACCATTTGAGTCCCTTTTACCGCTGTATACCA	1170
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Db	1172	ATTTTCTTTGTCTTTGGGTATACATTTTA	1201

ID	AAQ29104	standard; DNA; 1285 BP.
XX	AAQ29104;	
AC		
XX		
DT	25-MAR-2003 (updated)	
DT	24-FEB-1993 (first entry)	
XX		
DE	1psAg gene and u promoter.	
XX		
KM	Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;	
KM	vaccinia virus; hemorrhagic region; u; promoter; NYVAC; recombinant	
KM	HBV L; large pre-S antigen; 1psAg; fusion protein; pre-S region;	
KM	S12/core; S1; S2; Copenhagen vaccine strain; vaccinia virus;	
KM	virulence factor; deletion loci; recipient loci; ss.	
XX		
OS	Synthetic.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	CDS	116..1285
FT		/+tag= a
FT		/note= "1psAg gene"
FT	promoter	1..115

FT		/tag= b
FT		/note= "u promoter"
FT	misc_RNA	116..439
FT		/tag= c
FT	misc_RNA	/label= S1
FT		440..604
FT		/tag= d
FT	misc_RNA	/label= S2
FT		605..1282
FT		/tag= e
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XX		
PX	W09215672-A1.	
PD	17-SEP-1992.	
PF		
PF	09-MAR-1992;	92WO-US01906.
PR	07-MAR-1991;	91US-0666056.
PR	11-JUN-1991;	91US-0713967.
PR	06-MAR-1992;	92US-0847951.
PA	(VIRO-) VIROGENETICS CORP.	
PI	Cox WJ, De Taisne C, Francis J, Gettig R, Johnson GP;	
PI	Limbach KJ, Norton EK, Paoletti E, Perkins ME, Pincus SE;	
PI	Riviere M, Tartaglia J, Taylor J;	
DR	WPI: 1992-331718/40.	
DR	P-PADB; AAR27472.	
XX		
PT	Vaccine comprises recombinant, attenuated pox-virus - use for	
PT	vaccinating against viral infections such as rabies, hepatitis B,	
PT	HIV, HSV, EBV, CMV, mumps etc.	
XX		
PS	Disclosure: Fig 11; 456pp; English.	
XX		
CC	The sequence given encodes the hepatitis B virus (HBV) L protein	
CC	(large pre-S antigen, lpsAg) which is precisely linked to the cowpox	
CC	hemorrhagic region (u) promoter. This sequence was used in the	
CC	construction of a NYVAC recombinant expressing the HBV gene. Other	
CC	HBV genes were also used in the construction. These were HBV M	
CC	protein (small pre-S antigen, spsAg) and a fusion protein composed of	
CC	the entire pre-S region (S12/core, S1 + S2). Each of these gene	
CC	sequences were inserted individually into three different sites of	
CC	NYVAC separated by from each other by large regions of vaccinia DNA	
CC	containing essential genes. NYVAC is a Copenhagen vaccine strain of	
CC	vaccinia virus which has been modified by deletion of six non-essential	
CC	regions of the genome encoding known or potential virulence factors.	
CC	The deletion loci were engineered as recipient loci for the insertion	
CC	of foreign genes. The spacing of the three inserted sequences ensured	
CC	that any recombination that did occur would lead to disruption of the	
CC	vaccinia genome and would cause unviable vaccinia virus. See also	
CC	AA035501-864.	
CC	(Updated on 25-MAR-2003 to correct PN field.)	
SQ	Sequence 1285 BP; 284 A; 364 C; 272 G; 365 T; 0 other;	
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XX		
Query Match	94.6%; Score 1117.2; DB 13; Length 1285;	
Best Local Similarity	97.2%; Pred. No. 0;	
Matches 1137; Conservative	0; Mismatches 33; Indels 0; Gaps 0	
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Dd	116 ATGGGGCGAATCTTTTCCAGCAGCATCTCTGGGATTCTTCCGCAGCACCAAGTTGGAT	175
OY	61 CCAGCTTCAGAGCAAAACCAACAACATCCAGATTGGGACTTCAATCCCAACAGAACACC	120
Dd	176 CCAGCTTCAGAGCAAAACCAACAACATCCAGATTGGGACTTCAATCCCAACAGAACACC	235
OY	121 TTGGCACAAGCGCAACAAGGTGAGACTGGAGACATTCCGACTTGGGGTTTACCCACCGCAC	180
Dd	236 TTGGCACAAGCGCAACAAGGTGAGACTGGAGACATTCTGGGGTGGGTTTACCCACCGCAC	295

Oy	181	CGAGGCCCTTTGGGGTGGAGGCCCTCAGGCTCAGGGCATTAACAACAACCTTGCCCAAACT	240
Db	296	GGAGGCCCTTTGGGGTGGAGGCCCTCAGGCTCAGGGCATTAACAACCTTGCCCAAACT	355
Oy	241	CCGCCTCTGCTTCCACCAATCGCCAGTCAAGAAAGCAGCTTACC CGCTCTTCCAACT	300
Db	356	CCGCCTCTGCTCTCCACCAATCGCCAGTCAAGAAAGCAGCTTACC CGCTCTTCCAACT	415
Oy	301	TTGAGAAACACTCATCTCAAGCCATGCAGTGGAACTCCACAACCTTTCCACAACCTCTG	360
Db	416	TTGAGAAACACTCATCTCAAGCCATGCAGTGGAACTTTCCACAACCTTTCAACAACTCTG	475
Oy	361	CAAGATCCCAAGTGAAGAGCTGTGATTTCCCTGCTGGTGGCTCAGTTGAGAAACGTA	420
Db	476	CAAGATCCCAAGTGAAGAGCTGTGATTTCCCTGCTGGTGGCTCAGTTGAGAGCAGTA	535
Oy	421	AACCTGTTCGCACTACTGTCTCTCCATTCGTCATCTTTCTGAGGATTTGGGAGCCCT	480
Db	536	AACCTGTTCGCACTACTGTCTCTCCATTCGTCATCTTTCTGAGGATTTGGGAGCCCT	595
Oy	481	GCGGGAAACATGAGAACATCATCAGGAATTCTAGAACCCCTGCTCTGTTTACAGCG	540
Db	596	GCGGTGAACATGAGAAACATCATCAGGAATTCTAGAACCCCTCTGTGTACAGCG	655
Oy	541	GGGTTTTCTTGTGACAAAGATTCCTCAACATACCGCAAGCTAGATCTCGTGTGACT	600
Db	656	GGGTTCTTGTGTGACAAAGATTCCTCAACATACCGCAAGCTAGACTCTGTGTGACT	715
Oy	601	TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTTGGCCAAATTCGCACTCCCAAC	660
Db	716	TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTTGGCCAAATTCGCACTCCCAAC	775
Oy	661	TCCAATCACTACCAACCTCTGTCTCTCAACCTTGTCTCGTTATCGTGAATGTGTCTG	720
Db	776	TCCAATCACTACCAACCTCTGTCTCTCAACCTTGTCTCGTTATCGTGAATGTGTCTG	835
Oy	721	CGGGCTTTATCATCTTCCTCTTCATCCGCGCTGATACGCTCATTTCTGTGGTCTT	780
Db	836	CGGGCTTTATCATCTTCCTCTTCATCCGCGCTGATACGCTCATTTCTGTGGTCTT	895
Oy	781	CTGACTATCAAGGATGTGGCCGTTTGTCTCTTAATTCCAGATCTTCAACCAACGAC	840
Db	896	CTGACTATCAAGGATGTGTGGCCGTTTGTCTCTTAATTCCAGATCTTCAACCAACGAC	955
Oy	841	ACGGACCATGCAAGGCTGCAAGACTCTGTCAAGAACCTTAATGATTCCTCTCTGT	900
Db	956	ACGGACCATGCGAAGCTGCAAGACTCTGTCTCAAGAACCTTAATGATTCCTCTCTGT	1015
Oy	901	TGCTGTACAAAACCTTGGATGGAAGACACTGTATTTCCCATCCATCATCTCGAGCT	960
Db	1016	TGCTGTACAAAACCTTGGATGGAAGATTTGCAACTGTATTTCCCATCCATCATCTCGAGCT	1075
Oy	961	TTGCGAAAATTCCTATGGAAGTGGGCTCAGGCCGTTTCTCTGGCTCAGTTTACTAGTG	1020
Db	1076	TTGCGAAAATTCCTATGGAAGTGGGCTCAGGCCGTTTCTCTGGCTCAGTTTACTAGTG	1135
Oy	1021	CCATTGTTCAGTGGTGTGTAAGGCTTTCCCCACTGTTTGGCTTTCAAGTATATGATG	1080
Db	1136	CCATTGTTCAGTGGTGTGTAAGGCTTTCCCCACTGTTTGGCTTTCAAGTATATGATG	1195
Oy	1081	ATGTTGTACTGGGGGCAAGTGTATACACCATCTTGAGTCCCTTTTACCGCTGTATACA	1140
Db	1196	ATGTTGTATTTGGGGGCAAGTGTATACACCATCTTGAGTCCCTTTTACCGCTGTATACA	1255
Oy	1141	ATTTCTTTTGTCTTTGGGTATACATTTAA	1170
Db	1256	ATTTCTTTTGTCTTTGGGTATACATTTAA	1285

XX	AA	AN93072;
AC		
XX	DT	02-JUL-1990 (first entry)
XX		
XX	DE	Sequence encoding S1, S2 and S-genes of hepatitis B
XX	DE	
XX	XX	Hepatitis B; vaccine; pre-S component; ds.
XX	XX	
OS		Hepatitis B virus.
XX		
FH	Key	Location/Qualifiers
FT	CDS	12..382
FT		/*tag= a
FT		/label=S1 encoding sequence.
FT	CDS	383..500
FT		/*tag= b
FT		/label=S2 encoding sequence.
FT		501..2342
FT	CDS	/*tag= c
FT		/label=S encoding sequence.

/label=s encoding sequence.

W08810301-A.

29-DEC-1988.

22-JUN-1988;

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Query Match	Best Local Similarity	Matches 1148; Conservative	Score 94.6%; 97.1%;	Pred. No. 0;	Mismatches 33;	Indels 1;	Gaps 1;
1	ATGGGGCGAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCGACCAACGATTGGAT	60					
12	ATGGGGCGAATCTTTCCACGAGCAATCTCTGGGATTTCTTCCGACCAACGATTGGAT	71					
61	CCAGCTTCAGAGCAAAACCAACATTCAGATTGGGACCTTCAATCCCAACAGACACC	120					
72	CCAGCTTCAGAGCAAAACCAACATTCAGATTGGGACCTTCAATCCCAACAGACACC	131					
121	TGGCCAGACGCAACAAAGGTAGAGCTGAGGACATTTGGGACTGGGGTTACCCACGCGAC	180					
132	TGGCCAGACGCAACAAAGGTAGAGCTGAGGACATTTGGGACTGGGGTTACCCACGCGAC	191					
181	GGAGGCTTTTGGGGTGAGGCTTCAGGCTTCAGGCGCAATACACAACTTTCAGCAAAAT	240					
192	GGAGGCTTTTGGGGTGAGGCTTCAGGCTTCAGGCGCAATACACAACTTTCAGCAAAAT	251					
241	CGGCTCTCTGCTTCACCAATTCGCGAGTCAGAGAAAGGCAAGCTTACCCGCTGTCTTCACCT	300					
252	CGGCTCTCTGCTTCACCAATTCGCGAGTCAGAGAAAGGCAAGCTTACCCGCTGTCTTCACCT	311					

Db	1463	AAATCCAAAGTCAGGGGCTGTATTTCTCTGCTGGCTCAGATTCAAGGATAGTGA	1522
Qy	423	CCCTGTTCCGACTACTGTCTCTCCCATTCGTCAATCTTCTCGAGAGATTGGGGACCCCTGC	482
Db	1523	CCCTGTTCCGACTATTGCTCTCACAATCTCGTCATCTTCTCCAGAGATTGGGGACCCCTGC	1582
Qy	483	GCGGAACATGGAGAACATCATCATCAGAGATTCTTGAAGACCCCTGCTGTATTACAGCGGG	542
Db	1583	ACCGAACAATGGAGAACATCATCATCAGAGATTCTTGAAGACCCCTGCTGTATTACAGCGGG	1642
Qy	543	GTTTTTCTGTGTAAGAAGATCCTCAATATCCGAGACTTGAATCGTGGAGCTTC	602
Db	1643	GTTTTTCTGTGTAAGAAGATCCTCAATATCCGAGACTTGAATCGTGGAGCTTC	1702
Qy	603	TCTCAATTTTCTAGAGGGGAACTACCGTGTCTTGGCCAAAATTGCACTGCCCAACTTC	662
Db	1703	TCTCAATTTTCTAGAGGGGAGTCCCGTGTCTTGGCCAAAATTGCACTGCCCAACTTC	1762
Qy	663	CAATCACTACCAACCTCTGCTCTCCAACTTGTCTGTTATCGTGGATGTCTGCG	722
Db	1763	CAATCACTACCAACCTCTGCTCTCCAACTTGTCTGTTATCGTGGATGTCTGCG	1822
Qy	723	GCGTTTATCATCTTCTCTTATCCTGCTGATCGTGGATGTCTGTTATCGTGGATGTCTGCG	782
Db	1823	GCGTTTATCATATTCCTTCTTATCCTGCTGATCGCTCATCTTCTGTGTGTTCTTCT	1882
Qy	783	GGACTATCAAGGTATGTGCCCCGTTTGTCTCTAATTCAGAGATCTTCAACACACAGCAC	842
Db	1883	GGACTATCAAGGTATGTGCCCCGTTTGTCTCTAATTCAGAGATCTTCAACACACAGCAC	1942
Qy	843	GGAGACATGACAGACCTCTGACGACTCTGCTCAAGAGAACCTGTATTCCTCTGTTG	902
Db	1943	GGAGACCTGCAAAACCTGACGACTCTCTCAAGGCAACTATGTATCCCTCATGTTG	2002
Qy	903	CTGTATCAAAACCTTGGAGATGAGAACTGACCTGTATTCCTCAATCCATCTGCTGCTT	962
Db	2003	CTGTATCAAAACCTTGGAGAGAAATGACCTGTATTCCTCAATCTTGGGCTTT	2062
Qy	963	CGGAATAATTCCTATGGAGATGGGGCTCAGACCCGTTTCTCTGGCTCAGTTTACTAGTGC	1022
Db	2063	CGCAAAATATTCATATGGAGATGGGGCTCAGTCCGTTTCTCTGGCTCAGTTTACTAGTGC	2122
Qy	1023	ATTGTTCAGTGTGTTCTGTAAGGCTTCCCACTGTTTGGCTTCAATATATGATGAT	1082
Db	2123	ATTGTTCAGTGTGTTCTGTAAGGCTTCCCACTGTTTGGCTTCAATATATGATGAT	2182
Qy	1083	GTTGTACTGGGGGCCAAGTCTGTACACCATTTGAGTCCCTTTTACCGCTGTACCAAT	1142
Db	2183	GTTGTACTGGGGGCCAATCTGTACAAACCTTTGAGTCCCTTTTATACCGCTGTACCAAT	2242
Qy	1143	TTTTCTTTGTCTTTGGGTATACATTTTAAACCCATATAA	1181
Db	2243	TTTTCTTTGTCTTTGGGTATACATCTTAAACCCATATAA	2281
RESULT 9			
AAD09091			
ID AAD09091 standard; DNA; 3248 BP.			
XX	AC	AAD09091;	
XX	DT	04-SEP-2001 (first entry)	
XX	XX		
DE	XX	Hepatitis B virus FRI strain genotype G DNA.	
XX	XX		
XX	XX	HBV genotype G; precore; core antigen; HBsAg; HBpD; polymerase; preS1;	
KW	XX	envelope protein; preS2; surface antigen; HBsAg; HBx protein; vaccine;	
KW	XX	liver disease; hepatitis; liver cancer; circular; cyclic; ds.	
OS	XX	Hepatitis B virus.	
PI	XX		
DR	XX	Key Location/Qualifiers	
FT	CDS	1..675	
FT	FT	/tag= a	
FT	FT	/product= "PreCore/HBsAg core protein"	
FT	FT	/transl_except= (pos:4..6, aa:Xaa)	
FT	FT	/transl_except= (pos:82..84, aa:Xaa)	
FT	FT	/note= "Xaa corresponds to in-frame stop codon"	
FT	misc_feature	1..87	
FT	FT	/tag= b	
FT	FT	/note= "PreCore protein DNA"	
FT	FT	88..675	
FT	FT	/tag= c	
FT	FT	/note= "HBsAg core protein DNA"	
FT	FT	94..129	
FT	FT	/tag= d	
FT	FT	/note= "Core insert peptide DNA"	
FT	FT	530..3058	
FT	FT	/tag= e	
FT	FT	/product= "HBpD protein"	
FT	FT	1435	
FT	FT	/tag= f	
FT	FT	/note= "Corresponds to the end position (3248) of the circular HBV DNA"	
FT	FT	1436	
FT	FT	/tag= g	
FT	FT	/note= "Corresponds to the start position (1) of the circular HBV DNA"	
FT	FT	1071..2270	
FT	FT	/tag= h	
FT	FT	/product= "PreS1-PreS2-HBsAg envelope proteins"	
FT	FT	1071..1424	
FT	FT	/tag= i	
FT	FT	/product= "PreS1 envelope protein"	
FT	FT	/note= "Does not include stop codon"	
FT	FT	1425..1589	
FT	FT	/tag= j	
FT	FT	/product= "PreS2 envelope protein"	
FT	FT	/note= "Does not include stop codon"	
FT	FT	1590..2270	
FT	FT	/tag= k	
FT	FT	/product= "Hepatitis B surface antigen (HBsAg) protein"	
FT	FT	2809..25	
FT	FT	/tag= l	
FT	FT	/product= "HBx protein"	
FT	FT	/transl_except= (pos:3244..4, aa:Ala-Cys)	
FT	FT	/note= "The nucleotides 2809-3246 and 2-25 encode amino acids 1-146 and 147-153, respectively of the HBx protein (AAE04712)"	
FT	FT	3151..3246	
FT	FT	/tag= m	
FT	FT	/product= "HBx protein fragment (AAE04714)"	
FT	FT	/note= "Does not include start and stop codons"	
FT	FT	partial	
FT	FT	2..25	
FT	FT	/tag= n	
FT	FT	/product= "HBx protein fragment (AAE04713)"	
FT	FT	/note= "Does not include start codon"	
FT	FT	partial	
XX	XX		
XX	PN	W0200136498-A2.	
XX	PD	31-MAY-2001.	
XX	XX		
XX	PF	21-NOV-2000; 2000WO-US32108.	
XX	XX		
PR	XX	24-NOV-1999; 99US-0167206.	
XX	XX		
XX	PA	(PHAR-) PHARMASSET INC.	
XX	PA	(INNO-) INNOMENETICS NV.	
XX	XX	Sruyer L, Schinazi R, De Gendt S, Van Geyt C, Zoulim F, Fried M, Rossau R,	
PI	XX		
DR	XX	WPI; 2001-367676/38.	

PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
therapy

XX Claim 4; Fig 3, 94pp; English.

XX The invention relates to the complete nucleic acid sequence of a new
CC human hepatitis B virus (HBV) genotype, provisionally named genotype
CC G. This genotype was found with a high prevalence in patients
CC chronically infected with HBV and residing in Europe and the USA. The
CC invention relates to a fully defined sequence of 3248 nucleotides as
CC given in specification, a sequence with 92% identity to the given
CC sequence, or sequence that is degenerate to the mentioned sequences.
CC These polynucleotides are useful for HBV genotyping. The proteins
CC encoded by the polynucleotides are useful for detecting antibodies in
CC a biological sample. Ligands that bind to the proteins and antibodies
CC directed against the proteins are useful for detecting the proteins
CC and for detecting HBsAg and HBeAg (precore precursor proteins). They
CC are also useful for preparing a vaccine or medicament for treating
CC HBV infections. The present sequence is the complete coding
CC sequence of the HBV preS/S gene.

XX Sequence 1203 BP; 256 A; 353 C; 262 G; 328 T; 4 other;

Query Match 85.5%; Score 1010.2; DB 22; Length 1203;
Best Local Similarity 91.5%; Pred. No. 3,4e-307;
Matches 1069; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

```
QY 3 GGGGCAGAAATCTTCCACCAAGATCTCTGGGATTTCTTCCGACCAACCAAGTTGATCC 62
DB 36 GGGGAAACCTTTCCACCAAGATCTCTGGGATTTCTTCCGACCAACCAAGTTGATCC 95
QY 63 AGCCTTCAGAGCAAAACCAACCAATCCAGATTGGAGCTTCAATCCCAAGAGACACTG 122
DB 96 AGCATTGAGAGCAAAATCCAAACCAATCCAGATTGGAGCTTCAATCCCAAGAGACACTG 155
QY 123 GCCAGACGCCAAACAGGTAGAGCTGAGACTTGGACTGGGTTCAACCCGACGCGA 182
DB 156 GCCAGAGGCAAAACAGGTAGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAG 215
QY 183 AGGCTTTTGGGGTGGAGCCCTCAGCTCAGGGGATAACAAACCTTGGCAGCAATCC 242
DB 216 AGGCTTTTGGGGTGGAGCCCTCAGCTCAGGGGATAACAAACCTTGGCAGCAATCC 275
QY 243 GCCTCCTGCTTCCACCAATCCGAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 302
DB 276 GCCTCCTGCTTCCACCAATCCGAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 335
QY 303 GAGAAACACTCATCTCAAGCCATGCAAGTGAAGTCAACAACTTCCACCAACTTCA 362
DB 336 AAGAGACAGTCTCTCAAGCCATGCAAGTGAAGTCAACAACTTCCACCAACTTCA 395
QY 363 AGATCCCAAGTGAAGTCTGTATTTCCCTGCTGGTGGTCCAGTTCAAGAAAGTAAA 422
DB 396 AAGATCCCAAGTGAAGTCTGTATTTCCCTGCTGGTGGTCCAGTTCAAGAAAGTAAA 455
QY 423 CCCTGTTCCGAGTCTGTCTCCCATATGCTCAATCTTCCAGAGATTGGAGGAGCCCTGC 482
DB 456 CCCTGTTCCGAGTCTGTCTCCCATATGCTCAATCTTCCAGAGATTGGAGGAGCCCTGC 515
QY 483 GCGGAGACATGAGAAATCATACATGAGATTCTTGAAGACCCCTGCTGTGTTAAGGCGG 542
DB 516 ACCGAAATGAGAAATCATACATGAGATTCTTGAAGACCCCTGCTGTGTTAAGGCGG 575
QY 543 GTTTTCTGTGTGACAAAGATCTTCAAAATCCGCAAGTCTAAGCTGTGTGATCTTC 602
DB 576 GTTTTCTGTGTGACAAAGATCTTCAAAATCCGCAAGTCTAAGCTGTGTGATCTTC 635
QY 603 TCTCAATTTTCTAAGGAGAACTACAGTGTGCTTGGCCAAATTCGAGTCCCAACCTC 662
DB 636 TCTCAATTTTCTAAGGAGAACTACAGTGTGCTTGGCCAAATTCGAGTCCCAACCTC 695
QY 663 CAATCACTACCAACCTCTGCTCTCCAACTTGTCTGGTTATGCTGGATGTGTCTGCG 722
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DB 696 CAATCACTACCAACCTCTGCTCTCCAACTTGTCTGGTTATGCTGGATGTGTCTGCG 755
QY 723 GCGTTTATCATCTTCCTCTTCAACCTGAGTATGATGATCTCTCTGTGTGATCTCTC 782
DB 756 GCGTTTATCATCTTCCTCTTCAACCTGAGTATGATGATCTCTCTGTGTGATCTCTC 815
QY 783 GGAATTCAGATGATGTGCGCTTGTCTCTTAATTCAGATCTTCAACCAACCAAGAC 842
DB 816 GGAATTCAGATGATGTGCGCTTGTCTCTTAATTCAGATCTTCAACCAACCAAGAC 875
QY 843 GGAATTCAGATGATGTGCGCTTGTCTCTTAATTCAGATCTTCAACCAACCAAGAC 902
DB 876 GGAATTCAGATGATGTGCGCTTGTCTCTTAATTCAGATCTTCAACCAACCAAGAC 935
QY 903 CTGACCAAACTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 962
DB 936 CTGACCAAACTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 995
QY 963 CGGAAATTCCTATGAGAGTGGGCTCAGCCCTTCTCTCTGCTGCTGCTGCTGCTGCTG 1022
DB 996 CGGAAATTCCTATGAGAGTGGGCTCAGCCCTTCTCTCTGCTGCTGCTGCTGCTGCTG 1055
QY 1023 ATTTGTTCACTGTTGCTGAGGCTTTTCCCACTGTTGCTTCACTTCACTTCACTTCA 1082
DB 1056 ATTTGTTCACTGTTGCTGAGGCTTTTCCCACTGTTGCTTCACTTCACTTCACTTCA 1115
QY 1083 GTTGTACTGGGGGCAAGTGTATACACATCTGAGTCCCTTTTACCGCTGTACCAAT 1142
DB 1116 GTTGTACTGGGGGCAAGTGTATACACATCTGAGTCCCTTTTACCGCTGTACCAAT 1175
QY 1143 TTTCTTTTGTCTTGGGTATATATTTAA 1170
DB 1176 TTTCTTTTGTCTTGGGTATATATTTAA 1203
```

RESULT 11

AA005378 ID AA005378 standard; DNA; 3835 BP.

XX AA005378;

XX 10-DEC-1990 (first entry)

XX Sequence of hepatitis B genome.

XX tumorogenesis; vaccine; hepatitis; ds;

XX Hepatitis B virus.

XX JP02163089-A.

XX 22-JUN-1990.

XX 15-DEC-1988; 88JP-0315097.

XX 15-DEC-1988; 88JP-0315097.

XX (DAUC) DAICHI PHARM CO LTD.

XX WPI; 1990-235346/31.

XX HBV-DNA sequence and transgenic animal - used for screening for

XX hepatitis B-vaccine

XX Disclosure; Page 7; 7pp; Japanese.

XX Plasmid encoding HBV surface antigen (HBsAg) may be used to create a

XX transgenic animal expressing HBV DNA, useful in studying the mechanism

XX of tumourogenesis and assessing the effectiveness of Hep B vaccines.

XX Sequence 3835 BP; 825 A; 1048 C; 870 G; 1092 T; 0 other;

Query Match 85.1%; Score 1005; DB 11; Length 3835;
 Best Local Similarity 90.7%; Pred. No. 2.8e-305;
 Matches 1071; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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QY 1 ATGGGGGAGAAATCTTTCCACGAGCATCTCTGGGATTTCTTCCGACGACGAGTTGGAT 60
DB 1481 ATGGGAGAGAAATCTTTCTGTTCCCAATCTCTGGGATTTCTTCCGATACGAGTTGGAC 1540
QY 61 CCAGCCTTGAGAGCAAAACACCAATCCAGATTTGGGACTTCAATCCCAACAGAGACCC 120
DB 1541 CCGGCTTGAGAGCAAACTCACCAATCCGATTTGGGACTTCAATCCCAACAGAGATCAT 1600
QY 121 TGGCCAGAGCCGCAACAGGTAGAGCTGAGCATTTGGA CTGGGGTTCA CCCCACCGCAC 180
DB 1601 TGGCCAGAGGCAAAATAGGTAGAGGAGGAGCATTTGGGCTCAGGGTTCA CCCCACCGCAC 1660
QY 181 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGGATTAACAAACCTTTGCCAGCAAT 240
DB 1661 GGCGGCTTTTGGGGTGGAGCCCGCAGGCTCAGGGGATTTGA CAAACCGTGCAGTAGCA 1720
QY 241 CCGCCTCTGCTTCCACCAATCGCCAGTGAAGGAGGACCTTACCCGCTGTCTCCACCT 300
DB 1721 CCTCCTCCTGCTCCACCAATCGGAGTGAAGAGACGCTTACTCCATCTCTCCACCT 1780
QY 301 TTGAGAAACATCTCATCTCAAGCATGAGTGAACCTCCACAACTTTCCACAAACTCTG 360
DB 1781 CTAGAGAGACATCTCATCTCAGGCATGAGTGAACCTCCACAACTTTCCACAAAGCTCTG 1840
QY 361 CAAGATCCGAGAGTGAAGGCTGTATTTCCCTGCTGGTGGCTCCAGTTCCAGGAACAGTA 420
DB 1841 CTAGAGACCCGAGAGTGAAGGCGCTTATCTTCTGCTGGTGGCTCCAGTTCCGGAACAGTA 1900
QY 421 AACCTGTCTCCAGTACTGTCTCTCCCATATGTCATCTTTCGAGGATTTGGGGAGCCT 480
DB 1901 AACCTGTCTCCAGTACTGTCTCTCCCATATGTCATCTTTCGAGGATTTGGGGAGCCT 1960
QY 481 GCGGGAACATGAGAAACATCAATCAGGATTTCTAGGACCCCTGCTCGTTTACAGGCG 540
DB 1961 GCACCGAATGAGAAACATCAATCAGGATTTCTAGGACCCCTGCTCGTTTACAGGCG 2020
QY 541 GGGTTTTTCTTTGACAAAGATCTCTCAATACCGCAGAGTCTAGACTCTGTGTGAGT 600
DB 2021 GGGTTTTTCTTTGACAAAGATCTCTCAATACCGCAGAGTCTAGACTCTGTGTGAGT 2080
QY 601 TCTCTCAATTTCTAGGGGGAACCTACCGTGTCTTGGGCAAAATTTCCGAGTCCCAAC 660
DB 2081 TCTCTCAATTTCTAGGGGGAACCTACCGTGTCTTGGGCAAAATTTCCGAGTCCCAAC 2140
QY 661 TCCAACTCACTCAACACTCTGTCTCCAACTGTCTGTATTCGTGATGTGTCTG 720
DB 2141 TCCAACTCACTCAACACTCTGTCTCCAACTGTCTGTATTCGTGATGTGTCTG 2200
QY 721 CGGCGTTTATATCTTCTCTTCAATCTGTCTATGCTATGCTCATCTTCTTGTGTTCTT 780
DB 2201 CGGCGTTTATATCTTCTCTTCAATCTGTCTATGCTATGCTCATCTTCTTGTGTTCTT 2260
QY 781 CTGACATTCAGAGTATGTGCGCGTTGTCTCTAATTTCCAGATCTTCAACACACGAC 840
DB 2261 CTGACATTCAGAGTATGTGCGCGTTGTCTCTAATTTCCAGATCTTCAACACACGAC 2320
QY 841 ACGGAGCATGAGAGGCTGACAGACTCTGTCTCAAGGAACTCTATGATCCCTCCGTGT 900
DB 2321 ACGGAGCATGAGAGGCTGACAGACTCTGTCTCAAGGAACTCTATGATCCCTCCGTGT 2380
QY 901 TGTCTGACAAAACCTTTCGAGTGAACCTGACCTGTATTTCCATCCCATCTCTGGGT 960
DB 2381 TGTCTGACAAAACCTTTCGAGTGAACCTGACCTGTATTTCCATCCCATCTCTGGGT 2440
QY 961 TTGGGAAAATCTCTTATGAGAGTGGGCTTCAGCCGCTTCTCTGGCTAGTTACTAGTG 1020
DB 2441 TTGGGAAAATCTCTTATGAGAGTGGGCTTCAGCCGCTTCTCTGGCTAGTTACTAGTG 2500
QY 1021 CCATTTGTTCAGTGTTGTTAGGCTTTCCCACTGTGTTGGCTTTCAGTTATGATG 1080

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DB 2501 CCATTTGTTCAGTGTTGTTAGGCTTTCCCACTGTGTTGCTTTCAGTTATGATG 2560

QY 1081 ATGTGTACTGGGGGCAAGTGTGACACCAATCTAGACCTTTTTCACCGGTACCA 1140

DB 2561 ATGTGTATTTGGGGGCAAGTGTGACACCAATCTAGAGTCCCTTTTACCTTATTAACA 2620

QY 1141 ATTTCTTTTGTCTTGGGTATACATTTAAACCTATATAA 1181

DB 2621 ATTTCTTTTGTCTTGGGTATACATTTAAACCTATATAA 2661

RESULT 12
 AAD14316
 ID AAD14316 standard; DNA; 4084 BP.
 XX
 AC AAD14316;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Hepatitis B virus (HBV) 1.28 genome.
 XX
 KW Hepatitis B virus; HBV; altered sensitivity; agent; detection;
 KW PCR primer; Hepatitis B surface antigen; Hbsag; ds.
 XX
 OS Hepatitis B virus.
 XX
 PN W0200157244-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-AU00098.
 XX
 PA 03-FEB-2000; 2000US-0179948.
 XX
 PA (MELB-) MELBOURNE HEALTH.
 PA (PENN-) PENN STATE RES FOUND.
 XX
 PI Delaney W, Locarnini SA, Chen RYM, Bartholomeusz A, Isom H;
 XX
 DR WPI; 2001-496926/54.
 XX
 PT Detecting hepatitis B virus variant with altered sensitivity to agent,
 PT comprises infecting genetic construct containing replication competent
 PT genome to cells, contacting cells with agent and detecting replication
 PT of variant -
 XX
 PS Example 7; Fig 5A; 110bp; English.
 XX
 CC The invention relates to a method of detecting variant hepatitis B virus
 CC (HBV) which exhibits altered sensitivity to agents. The method involves
 CC infecting a genetic construct containing a replication competent amount
 CC of the genome from variant HBV contained in or fused to a baculovirus
 CC genome; contacting cells with the agent to be tested; culturing cells
 CC under conditions sufficient for the variant HBV to replicate, express
 CC genetic sequences, and/or assemble, and/or release viral particles; and
 CC determining replication of variant HBV using viral-component-detection
 CC means. The method is useful for detecting variant HBV which exhibits
 CC altered sensitivity to agents. The present sequence is the HBV 1.28
 CC genome.
 XX
 SQ Sequence 4084 BP; 920 A; 1105 C; 914 G; 1145 T; 0 other;

Query Match 84.8%; Score 1001.8; DB 22; Length 4084;
 Best Local Similarity 90.5%; Pred. No. 2.9e-304;
 Matches 1069; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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QY 1 ATGGGAGAGATCTTTTCCACGAGATCTCTGGATTTCTTCCGACGACGAGTTGAT 60
DB 1436 ATGGGAGAGATCTTTTCTGTTCCCAACCTCTGGGATTTCTTCCGATCATGAGTTGAC 1495
QY 61 CCAGCCTTGAGAGCAAAACACCAATCCAGATTTGGGACTTCAATCCCAACAGGAGACCC 120

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D 1496 CTGATTCGAGACCACTCAACATTCAGATTGGAGCTTCAACCCCATCAAGACAC 1555
Q 121 TGGCCAGACCCCAACAGGTAGAGCTGAGCATTTGGAGTTCACCCACCGCAC 180
D 1556 TGGCCAGACCCCAACAGGTAGAGGTGAGCATTTGGAGTTCACCCACCGCAC 1615
Q 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCACTTAACAACTTTGCCAGCAAT 240
D 1616 GGGGATTTTGGGGTGAAGCCCTCAGGCTCAGGGCACTTAAGACACAGTGTCAACAAT 1675
Q 241 CCGCTTCCTGCTTCCACCAATCGCCAGTCAGAAAGCAGCCCTACCGCTGCTCCACT 300
D 1676 CTTCTCTCTGCTTCCACCAATCGCCAGTCAGAAAGCAGCCCTACCGCTGCTCCACT 1735
Q 301 TTGAGAAACATCTATCTTCAAGCCATGACAGTGAACCTCCCAACTTTCCCAACACTG 360
D 1736 CTAAAGAACAGTCATCTCAGGCGCATGAGTGAATTCAGTGTTCACCAAGCTCTG 1795
Q 361 CAAGATCCCAAGAGTGAAGGTCTGTATTTCCCTGCTGAGCTCAGTTGAGAACAGTA 420
D 1796 CAGATCCCAAGAGTGAAGGTCTGTATTTCCCTGCTGAGCTCAGTTGAGAACAGTA 1855
Q 421 AACCTGTTCGACTACTGTCTCTCCATATCGTAATCTTCTGAGGATTTGGGACCT 480
D 1856 AACCTGTTCGACTACTGTCTCTCCATATCGTAATCTTCCGAGAGACTGGGGACCT 1915
Q 481 GCGGGAAACATGGAACATCATCATAGATTCCTAGAGCCCTGCTCGTTTACAGGCG 540
D 1916 GTGACGAACATGGAACATCATCATAGATTCCTAGAGCCCTGCTCGTTTACAGGCG 1975
Q 541 GGGTTTTCTTGTGACAGAATCTCTCAATACCGAGAGTCAGATCGTGTGACT 600
D 1976 GGGTTTTCTTGTGACAGAATCTCTCAATACCGAGAGTCAGATCGTGTGACT 2035
Q 601 TCTCTCAATTTTCTAGGAGGAACTACCGTGTCTTGGCCAAATTTGCGAGTCCCAAC 660
D 2036 TCTCTCAATTTTCTAGGAGGAACTACCGTGTCTTGGCCAAATTTGCGAGTCCCAAC 2095
Q 661 TCCAAATACATCACCACTCTCTGCTCCCACTTGTCTGTGATTCCTGATGATGCTG 720
D 2096 TCCAAATACATCACCACTCTCTGCTCCCACTTGTCTGTGATTCCTGATGATGCTG 2155
Q 721 CGGGCTTTTATCATCTTCTCTTCATCTGCTGCTAGTCCATCTTCTTGTGTTCTT 780
D 2156 CGGGCTTTTATCATCTTCTCTTCATCTGCTGCTAGTCCATCTTCTTGTGTTCTT 2215
Q 781 CTGAGATCAAGATATGTTGCCGTTTGTCTCTAATTCAGATCTTCAACCAACAGC 840
D 2216 CTGAGATCAAGATATGTTGCCGTTTGTCTCTAATTCAGATCAACCAACAGC 2275
Q 841 ACCGGACATGCAAGCTGACAGCTCTGCTCAAGGAACCTGATGATCCCTCGCT 900
D 2276 ACCGGACATGCAAGCTGACAGCTCTGCTCAAGGAACCTGATGATCCCTCGCT 2335
Q 901 TGCTGTACAAAACTTGGATGAAATGCACTGTATTTCCATCCCATCTCTGAGCT 960
D 2336 TGCTGTACAAAACTTGGATGAAATGCACTGTATTTCCATCCCATCTCTGAGCT 2395
Q 961 TTGGGAAATTTCTATGAGAGTGAGGCTCAGCCCGTTTCTCTGCTCAGTTTACTAGT 1020
D 2396 TTGGGAAATTTCTATGAGAGTGAGGCTCAGCTCGTTTCTCTGCTCAGTTTACTAGT 2455
Q 1021 CCATTTGTTCAGTGTCTGTAGGCTTCCCACTGTGTTGGCTTTCAGTTATATAGATG 1080
D 2456 CCATTTGTTCAGTGTCTGTAGGCTTCCCACTGTGTTGGCTTTCAGTTATATAGATG 2515
Q 1081 ATGTTGTACTGGGGCCAAGTCTGTACACATCTTGAATCCCTTTTACCGCTGTACA 1140
D 2516 ATGTTGTACTGGGGCCAAGTCTGTACACATCTGAGATCCCTTTTATACCGCTGTACA 2575
Q 1141 ATTTTCTTTTGTCTTGGGTATACATTTAAACCTTAATAA 1181
D 2576 ATTTTCTTTTGTCTTGGGTATACATTTAAACCTTAATAA 2616
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RESULT 13
AADI4317
ID AADI4317 standard; DNA; 4496 BP.
XX
AC AADI4317;
XX
DT 06-NOV-2001 (first entry)
XX
DE Hepatitis B virus (HBV) 1.5 genome.
XX
KM Hepatitis B virus; HBV; altered sensitivity; agent; detection;
XX PCR primer; Hepatitis B surface antigen; HBsAg; ds.
OS Hepatitis B virus.
XX
PN WO200157244-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001MO-AU00098.
XX
PR 03-FEB-2000; 2000US-0179948.
XX
PA (MELB-) MELBOURNE HEALTH.
XX (PENN-) PENN STATE RES FOUND.
XX
PI Delaney W, Locarnini SA, Chen RYM, Bartholomew A, Isom H;
XX
DR WPI; 2001-496926/54.
XX
PT Detecting hepatitis B virus variant with altered sensitivity to agent,
PT comprises infecting genetic construct containing replication competent
PT genome to cells; contacting cells with agent and detecting replication
PT of variant.
XX
PS Example 7; Fig 5B; 110bp; English.
XX
CC The invention relates to a method of detecting variant hepatitis B virus
CC (HBV) which exhibits altered sensitivity to agents. The method involves
CC infecting a genetic construct containing a replication competent amount
CC of the genome from variant HBV contained in or tested to a baculovirus
CC genome; contacting cells with the agent to be tested; culturing cells
CC under conditions sufficient for the variant HBV to replicate, express
CC genetic sequences, and/or assemble, and/or release viral particles; and
CC determining replication of variant HBV using viral component-detection
CC means. The method is useful for detecting variant HBV which exhibits
CC altered sensitivity to agents. The present sequence is the HBV 1.5
CC genome.
XX
SQ Sequence 4496 BP; 999 A; 1229 C; 1011 G; 1257 T; 0 other;
XX
Query Match 84.8%; Score 1001.8; DB 22; Length 4496;
Best Local Similarity 90.5%; Pred. No. 3.1e-304;
Matches 1069; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
Q 1 ATGGGCGAATCTTTCCACACGATCTCTGGAGTTCTTCCGACCAACAGTGGAT 60
D 1848 ATGGGCGAATCTTTCTGTTCCCAACCTCTGGAGTTCTTCCGATTCAGTTGGAC 1907
Q 61 CCAGCTTTCAGAGCAACCAACAAATCCAGATTGGGACTTTCATCCCAACAGACACC 120
D 1908 CTGCAATTCGAGGCAACCACTMAACAATCCAGATTGGGACTTTCATCCCAACAGACACC 1967
Q 121 TGGCCAGACCCCAACAGGTAGAGCTGAGCATTTGGAGTTCACCCACCGCAC 180
D 1968 TGGCCAGACCCCAACAGGTAGAGGTGAGCATTTGGGCTCAGCCCTCCACAC 2027
Q 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCACTTAACAACTTTGCCAGCAAT 240
D 2028 GGAGGATTTTGGGGTGAAGCCCTCAGGCTCAGGGCACTTAATGACACAGTGTCAACAAT 2087
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QY 241 CCGCTCTGCTCCACCAATGCGAGTCAAGAGGACCTAACCCGCTGTCTCCACT 300
DB 2088 CCTCTCTCCGCTCCCACTAGCGAGTCAGAGAGGACACTACTCTCTCCACT 2147
QY 301 TTGAGAAACATCATCTTCAAGCCATGAGTGAAGTCTCCAACTTTCCACCAACTCTG 360
DB 2148 CTAAGAGAGATCTCTCAGGCTCAGTCAAGTGAATTCACGCTTCCACCAAGTCTG 2207
QY 361 CAAGATCCAGAGTGAAGTCTGTATTTCCCTGCTGAGTCTCCAGTTCAAGAAACAGTA 420
DB 2208 CAGGATCCAGAGTCAAGGCTGTATTTCTTCTGCTGAGTCTCCAGTTCAAGAAACAGTA 2267
QY 421 AACCTGTTCGACTACTGTCTCTCCATATGCTCAATCTTTCGAGATTTGGGACCT 480
DB 2268 AACCTGTTCGAAATATGCTCTCTCAATCTGCTCAATCTCCGCGAGAGCTGGGACCT 2327
QY 481 GGGCGGACATGAGAAACATCATATGAGATTTCTTAGAACCCCTGCTGCTTTACAGGG 540
DB 2328 GTAGGAAATGAGAAACATCATATGAGATTTCTTAGAACCCCTGCTGCTTTACAGGG 2387
QY 541 GGGTTTTTCTTGTGAAGAATCTCAGCAATACCGCAGAGTCTAGACTCGTGTGAGT 600
DB 2388 GGGTTTTTCTTGTGAAGAATCTCAGCAATACCGCAGAGTCTAGACTCGTGTGAGT 2447
QY 601 TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTTCCGAGTCCCAAC 660
DB 2448 TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTTCCGAGTCCCAAC 2507
QY 661 TCCATCATCTCAACCACTCTCTCTCTCAATCTGCTATGCTATGCTATGCTATGCTAT 720
DB 2508 TCCATCATCTCAACCACTCTCTCTCTCAATCTGCTATGCTATGCTATGCTATGCTAT 2567
QY 721 CGGCGTTTTATCATCTCTCTCTCAATCTGCTATGCTATGCTATGCTATGCTAT 780
DB 2568 CGGCGTTTTATCATCTCTCTCTCAATCTGCTATGCTATGCTATGCTATGCTAT 2627
QY 781 CTGACTATCAAGATATGTTGCCGTTTGTCTCTAATTCAGATCTTCAACCAACAGC 840
DB 2628 CTGACTATCAAGATATGTTGCCGTTTGTCTCTAATTCAGATCTTCAACCAACAGC 2687
QY 841 ACGGACCTCAAGAGCTCTGACAGTCTCTGCTCAAGAACTCTATGATCTCTCTCT 900
DB 2688 ACGGACCTCAAGAGCTCTGACAGTCTCTGCTCAAGAGCTCTATGATCTCTCTCT 2747
QY 901 TSCGTGACAAAACCTTCGATGAGAACTGACCTGATTCCTCATCCATCATCTCGGCT 960
DB 2748 TSCGTGACAAAACCTTCGATGAGAACTGACCTGATTCCTCATCCATCATCTCGGCT 2807
QY 961 TTCGAAAATTCCTATGAGAGTGGGCTCAGCCGTTTCTCTGCTCAGTTTACTAGT 1020
DB 2808 TTCGAAAATTCCTATGAGAGTGGGCTCAGCCGTTTCTCTGCTCAGTTTACTAGT 2867
QY 1021 CCATTTGTCAGTGTCTGTAAGGCTTTCCCACTGTTTGTGCTTCACTTATATGATG 1080
DB 2868 CCATTTGTCAGTGTCTGTAAGGCTTTCCCACTGTTTGTGCTTCACTTATATGATG 2927
QY 1081 ATGTGTCTGAGGGGCAAGTCTGTAACACATCTGAGCCCTTTTACCGCTGTACCA 1140
DB 2928 ATGTGTCTGAGGGGCAAGTCTGTAACACATCTGAGCCCTTTTACCGCTGTACCA 2987
QY 1141 ATTTCTTTTGTCTTGGGTATACATTTAAACCTTATATA 1181
DB 2988 ATTTCTTTTGTCTTGGGTATACATTTAAACCTTATATA 3028

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RESULT 14
AAT36611
ID AAT36611 standard; cDNA; 1200 BP.

AC AAT36611;
XX
XX 25-MAR-2003 (updated)
DT 22-OCT-1996 (first entry)

```

XX DE Hepatitis B virus pre S1/pre S2/S gene (adr-1).
XX KW Hepatitis C virus; HCV; hepatitis B virus; HBV; fusion protein;
XX KW immunisation; vaccine; infection; core protein; adr-1; ds.
XX OS Hepatitis B virus.
XX FH Key
XX FT misc_difference 151..153
XX FT /tag= a
XX FT /transl_except= 151..153,aa:His
XX FT misc_difference 163..165
XX FT /tag= b
XX FT /transl_except= 161..163,aa:Ala
XX FT misc_difference 273..275
XX FT /tag= c
XX FT /transl_except= 273..275,aa:Val
XX PN WO9610997-A1.
XX PD 18-APR-1996.
XX PF 05-OCT-1995; 95WO-US13552.
XX PR 06-JUN-1995; 95US-0467859.
XX PR 05-OCT-1994; 94US-0318248.
XX PA (APOL-) APOLLON INC.
XX PA (GENO-) GEN HOSPITAL CORP.
XX PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
XX PI Coney LR, Pachuk CJ, Tokushige K, Wakita T, Wands J;
XX PI Zurawski VR;
XX DR WPI; 1996-209642/21.
XX DR P-PSDB; AAR93801.
XX PT Nucleic acid encoding hepatitis B and C virus fusion proteins - or
XX PT incomplete hepatitis C virus genome, are useful in vaccines for
XX PT prevention or treatment of HBV and HCV infections
XX PS Example 1; Page 32-34; 53pd; English.
XX CC A new fusion protein comprises a hepatitis B virus (HBV) S gene
XX CC protein (AAT36611) coupled to amino acids 1-69, 1-70 or 1-154 of the
XX CC hepatitis C virus (HCV) core protein (AAT28348).
XX CC The nucleic acid has the coding sequence linked to a CMV promoter,
XX CC RSV enhancer, polyadenylation sequence and opt. the 5'-UTR of HCV.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
SQ Sequence 1200 BP; 255 A; 351 C; 265 G; 329 T; 0 other:
Query Match 84.7%; Score 1000.6; DB 17; Length 1200;
Best Local Similarity 91.1%; Pred. No. 3.6e-304;
Matches 1063; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 1 ATGGGCGAAGATCTTCCACAGCAATCTCTGGAATCTTCCGACCAAGTTGAT 60
DB 34 ATGGGCGAAGATCTTCTGTTCCCAATCTCTGGGAATCTTCCGATCACCAGTTGAC 93
QY 61 CCAGCTTCAGAGCAACCAACCAATCCAGATTGGGACTTCATCCCAAGGACACC 120
DB 94 CCGCTTCAGAGCAACCAATCCAGATTGGGACTTCAGATTGGGACTTCAGATTGGG 153
QY 121 TGGCCAGACGCCCAACAGATGAGCTGAGCACTTGGAGTCTGAGGCTTACCCACG 180
DB 154 TGGCCAGAGGAATTAAGATGAGAGCGGAGACTTGGGCGCAGGCTTACCCACAC 213
QY 181 GGAGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCATTAACAAACCTTGGCAGCA 240
DB 214 GGCGGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCATTAATGACAAACAGTGCAG 273

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QY 241 CCGCCTCTCTCTCCACCAATCCGCACTCAGAAAGGAGCCCTACCCGCTGTCTCCACT 300
DB 274 CCTCTCTCTCTCTCCACCAATCCGCACTCAGAAAGGAGCCCTACCTCTCTCTCTCCACT 333
QY 301 TTGAGAAACACTACTCTCTCAAGCCATGCACTGGAACCTCCCAACTTTTCCCAAACTCTG 360
DB 334 CTAGAGACAGTCATCTCTCAGGCCATCAGTGAACCTCCCAAACTTTTCCCAAACTCTG 393
QY 361 CAAGATCCCAAGTGAAGGCTGTATTTCTCTGCTGGTGGCTCAGTTAGAGAACAGTA 420
DB 394 CTAGATCCCAAGTGAAGGCTGTATTTCTCTGCTGGTGGCTCAGTTAGAGAACAGTA 453
QY 421 AACCTGTTCGACTACTGTCTCTCCCAATCTCTCAATCTTTCTGAGAGATTGGGACCT 480
DB 454 AACCTGTTCGACTACTGTCTCTCCCAATCTCTCAATCTTTCTGAGAGATTGGGACCT 513
QY 481 GCGCGGAACATGAGAACATCATTCAAGATTTCTAGAGCCCTGCTGCTGTTTCAAGCG 540
DB 514 GCACCGAACAATGAGAGACACAAATCAGATTCCTTAGAGCCCTGCTGCTGTTTCAAGCG 573
QY 541 GGGTTTTCTTGTGACAAAGATCTCACAATACCGAGAGTCTAGACTGCTGGTGGACT 600
DB 574 GGGTTTTCTTGTGACAAAGATCTCACAATACCGAGAGTCTAGACTGCTGGTGGACT 633
QY 601 TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTTGCACTCCCAACC 660
DB 634 TCTCTCAATTTTCTAGGGGGAACCTACCGTGTCTTGGCCAAATTTGCACTCCCAACC 693
QY 661 TCCAAATCTCACCACCTCTCTCTCTCAACTTGTCTGTTATTCCTGGATGTCTGCTG 720
DB 694 TCCAAATCTCACCACCTCTCTCTCTCAACTTGTCTGTTATTCCTGGATGTCTGCTG 753
QY 721 CGCGCTTTTATCAATCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 754 CGCGCTTTTATCAATCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
QY 781 CTGAGACTATCAAGGATATGTGCGCGTGTCTCTCAATTTCCAGAGATTTCAACCAACAGC 840
DB 814 CTGAGACTATCAAGGATATGTGCGCGTGTCTCTCAATTTCCAGAGATTTCAACCAACAGC 873
QY 841 ACGGAGCAATGCAAGGCTGCAAGCTCTCTCTCTCAAGAACTTATGATTCCTCTCTGT 900
DB 874 ACGGAGCAATGCAAGGCTGCAAGCTCTCTCTCTCAAGAACTTATGATTCCTCTCTGT 933
QY 901 TGCTGTCAAAACCTTCTGATGGAACCTGCACTGTATTCCTATCCCATCATCTTGGGCT 960
DB 934 TGCTGTCAAAACCTTCTGATGGAACCTGCACTGTATTCCTATCCCATCATCTTGGGCT 993
QY 961 TTGGAAGAAATTCCTATGGAAGTGGGCTCAAGCCGTTTCTCTGGCTCAGTTTACTAGTG 1020
DB 994 TTGGAAGAAATTCCTATGGAAGTGGGCTCAAGCCGTTTCTCTGGCTCAGTTTACTAGTG 1053
QY 1021 CCATTTTCTCAGTGGTCTGTAAGGCTTTCCCGCACTGTTTGGCTTCAAGTTATATGATG 1080
DB 1054 CCATTTTCTCAGTGGTCTGTAAGGCTTTCCCGCACTGTTTGGCTTCAAGTTATATGATG 1113
QY 1081 ATGTTGACTGAGGGGCAAGTCTGTACACCACTTGAAGTCCCTTTTACCGCTGTACCA 1140
DB 1114 ATGTTGACTGAGGGGCAAGTCTGTACACCACTTGAAGTCCCTTTTACCGCTGTACCA 1173
QY 1141 ATTTTCTTTTGTCTTTGGGTATACATT 1167
DB 1174 ATTTTCTTTTGTCTTTGGGTATACATT 1200

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RESULT 15

AA23282 standard; DNA; 9325 BP.

AA23282:

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XX
AC
XX
XX
DT 31-JAN-2000 (first entry)
XX

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DE DNA sequence of plasmid pTHBV-d.
XX
XX Hepatitis B virus; HBV; recombinant; pol gene; X gene; surface antigen;
KM liver; anti-viral; anti-tumor; gene therapy; single-gene defect;
KM genetic disorder; familial hypercholesterolemia; neoplastic gene;
KM ornithine transcarbamylase deficiency; ss.
XX
OS Synthetic.
OS Hepatitis b virus.
XX
XX US981274-A.
XX
XX 09-NOV-1999.
XX
XX 18-SEP-1996; 96US-0715808.
XX
XX 18-SEP-1996; 96US-0715808.
XX
XX (CHAI/) CHAISOMCHIT S.
XX (CHAN/) CHANG L.
XX (TYRR/) TYRRELL D L J.
XX
XX Chang L, Chaiemchit S, Tyrrell DLJ;
PI WPI; 1999-633330/54.
XX
XX Recombinant hepatitis B virus genome containing heterologous gene
XX sequences useful for treating liver infections -
XX
XX Example 1; Columns 39-48; 53bp; English.
XX
XX The invention relates to a recombinant hepatitis B virus genome (HBV)
XX that comprises heterologous gene sequences which express at least one
XX functional heterologous gene product. A host cell transfected with a
XX recombinant HBV genome comprising pol gene sequences, X gene sequences
XX and surface antigen gene (preS1/preS2/S gene) sequences and heterologous
XX CC gene sequences can be used to express at least one functional
XX CC heterologous gene product. The invention also provides a method for
XX CC encapsidating a recombinant HBV genome. The recombinant HBV genomes are
XX CC useful for the expression of functional heterologous gene products in
XX CC liver cells. The vectors can be used for anti-viral, anti-tumor and/or
XX CC gene therapy and particularly for the correction of inherited single-gene
XX CC defects. Human genetic disorders which can be treated by expression of
XX CC missing or mutant genes in the liver are familial hypercholesterolemia
XX CC and ornithine transcarbamylase deficiency. Primary tumors of the liver.
XX CC may benefit from the expression of anti-neoplastic genes in the liver.
XX CC Existing retroviral vectors and other animal viruses which are used to
XX CC deliver foreign genes are not liver-specific with regard to their
XX CC infection or expression unlike hepatitis B viral vectors. Human hepatitis
XX CC B virus can be delivered through the circulation so there is no
XX CC requirement for tissue culture for ex vivo liver-directed gene therapy.
XX CC The present sequence represents the DNA sequence of the plasmid pTHBV-d
XX CC which comprises HBV sequences.
XX
XX
SQ Sequence 9325 BP; 2227 A; 2448 C; 2132 G; 2518 T; 0 other;
XX
XX
Query Match 84.7%; Score 1000.2; DB 20; Length 9325;
Best Local Similarity 90.4%; Pred. No. 1.5e-303;
Matches 1068; Conservative 0; Mismatches 113; Indels 0; Gaps 0;
QY 1 ATGGGGGAGAAATCTTTCACAGCAATCTCTGGGAATCTTTCGACACCAAGTTGGAT 60
DB 3135 ATGGGGGAGAAATCTTTCGTCCAATCTCTGGGAATCTTTCGACATCATGTTGGAC 3194
QY 61 CCAGCTTTCAGAGCAACACCAATCCAGATTTGGGACTTCAATCCCAACAGACACC 120
DB 3195 CTTGCAATTCGAGACCAACTCAATCCAGATTTGGGACTTCAACCCGTCAGAGAC 3254
QY 121 TGGCAGACGCGCAACAGGATGAGGCTGAGCAATTCGAGACTGGGGTTTCAACCCGAC 180
DB 3255 TGGCAGACGCGCAACAGGATGAGGCTGAGCAATTCGAGACTGGGGTTTCAACCCG 3314
QY 181 GAGAGCCTTTTGGGGTGAACCTCTCAGGCTCAGGGCATACACAAACCTTTCAGCAAA 240

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Db 3315 GGGGATTTTGGGGTGGAGGCGCTCAGGCTCAGGGCATATTGACCAAGTTCACACATT 3374
QY 241 CCGCTCTGCTCTCCACCAATCGCCAGTGAAGGAGCGCTACCCCGCTGTCTCCACCT 300
Db 3375 CCGCTCTGCTCTCCACCAATCGCCAGTGAAGGAGCGCTACCCCGCTGTCTCCACCT 3434
QY 301 TTGAGAACATCATCTCTCAAGCCATGCACTGGAACCTCCACAACTTTCACCAACTCTG 360
Db 3435 CTAAAGAGACAGTATCTCTCAGGCCATGCACTGGAATTCACCTGCTTCCACCAACTCTG 3494
QY 361 CAAGATCCCAAGTGAAGGTCTGTATTCTCTGCTGTGTGCTCCAGTTCAGGACAGTA 420
Db 3495 CAGGATCCCAAGTGAAGGTCTGTATTCTCTGCTGTGTGCTCCAGTTCAGGACAGTA 3554
QY 421 AACCTGTTCGCACTGCTCTCCCATATGCTCATCTTTCGAGGATTTGGGACCCCT 480
Db 3555 AACCTGTTCGCACTGCTCTCCCATATGCTCATCTTTCGAGAGACTGGGGACCCCT 3614
QY 481 GCGCGGACATGAGAACATCATGAGATTCCTAGAACCCCTGCTGTGTTCAGAGCG 540
Db 3615 GTGACGACATGAGAACATCATGAGATTCCTAGAACCCCTGCTGTGTTCAGAGCG 3674
QY 541 GGGTTTTTCTGTGACAGAAATCTCACAATACCGAGAGTCTAGACTGTGTGACT 600
Db 3675 GGGTTTTTCTGTGACAGAAATCTCACAATACCGAGAGTCTAGACTGTGTGACT 3734
QY 601 TCTCTAATTTTCTAGGGGGAACTACGGTGTCTTGGCCAAATTCGAGTCCCAACC 660
Db 3735 TCTCTAATTTTCTAGGGGGATCTCCGGTGTCTTGGCCAAATTCGAGTCCCAACC 3794
QY 661 TCCAACTACTCAACCACTCTGTCTCTCAACTTGTCTGTATGCTGATGTGTCTG 720
Db 3795 TCCAACTACTCAACCACTCTGTCTCTCAACTTGTCTGTATGCTGATGTGTCTG 3854
QY 721 CCGCGTTTATCATCTTCTCTCTCATCTGCTGTCTATGCTCTCATCTTGTGTCTT 780
Db 3855 CCGCGTTTATCATCTTCTCTCTCATCTGCTGTCTATGCTCTCATCTTGTGTCTT 3914
QY 781 CTGCACTATCAAGGTATGTTGGCCGTTTGTCTTAATTCAGAGATCTTCAACCAACGCG 840
Db 3915 CTGCACTATCAAGGTATGTTGGCCGTTTGTCTTAATTCAGAGATCTTCAACCAACGCG 3974
QY 841 ACGGACCATGAGAGCTGCAAGCTCTGCTCAAGAACTCTATGTATCCCTCTGT 900
Db 3975 ACGGACCATGAGAACTGCAAGCTCTGCTCAAGCACTCTATGTTCCCTCATGT 4034
QY 901 TGTGTACAAAACCTTGGATGGAACCTGACCTGTATTCCATCCCATCATCTGCGCT 960
Db 4035 TGTGTACAAAACCTTGGATGGAATTCGACCTGTATTCCCATCATCTGCGCT 4094
QY 961 TTGGAAAAATTCCTATGAGGAGTGGGCTCAGCCCGTTTCTCTGCTCAGTTTACTAGTG 1020
Db 4095 TTGGAAAAATTCCTATGAGGAGTGGGCTCAGTCCGTTTCTCTGCTCAGTTTACTAGTG 4154
QY 1021 CCATTGTTCAGTGTTCGTAGGGCTTTCGCCACTGTTGGCTTCAGTTATATGATG 1080
Db 4155 CCATTGTTCAGTGTTCGTAGGGCTTTCGCCACTGTTGGCTTCAGTTATATGATG 4214
QY 1081 ATGTGTACTGGGGGCAAGTCTGTACACCATCTTGATCCCTTTTACCGCTGTACCA 1140
Db 4215 ATGTGTATTTGGGGGCAAGTCTGTACACCATCTTGATCCCTTTTACCGCTGTACCA 4274
QY 1141 ATTTCTTTTGTCTTTGGGTATACATTAAACCTTAATAA 1181
Db 4275 ATTTCTTTTGTCTTTGGGTATACATTAAACCTTAACAA 4315

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OM nucleic - nucleic search, using sw model

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(without alignments)
7239.909 Million cell updates/sec

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Perfect score: 1181
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1117.2	94.6	1201	1	US-08-105-483-218 Sequence 218, App
2	1117.2	94.6	1201	1	US-08-709-209-218 Sequence 218, App
3	1117.2	94.6	1201	1	US-08-458-101-218 Sequence 218, App
4	1117.2	94.6	1285	1	US-08-105-483-215 Sequence 215, App
5	1117.2	94.6	1285	1	US-08-709-209-215 Sequence 215, App
6	1117.2	94.6	1285	1	US-08-458-101-215 Sequence 215, App
7	1088.2	92.1	2348	3	US-08-480-173A-42 Sequence 42, Appl
8	1088.2	92.1	2348	3	US-08-484-408A-42 Sequence 42, Appl
9	1000.6	84.7	1200	3	US-08-854-531-5 Sequence 5, Appl
10	1000.6	84.7	1200	3	PCT-US95-13553-5 Sequence 5, Appl
11	1000.2	84.7	9325	2	US-08-715-808-2 Sequence 2, Appl
12	1000.2	84.7	9659	2	US-08-715-808-6 Sequence 6, Appl
13	988.2	83.7	3220	6	5196194-15 Patent No. 5196194
14	985.8	83.5	7463	2	US-08-715-808-13 Sequence 13, Appl
15	811.2	68.7	3182	4	US-08-890-735C-1 Sequence 11, Appl
16	810.8	68.7	846	4	US-09-247-890-11 Sequence 11, Appl
17	810.8	68.7	846	4	US-09-724-969-11 Sequence 11, Appl
18	810.8	68.7	846	4	US-09-724-852-11 Patent No. 5164485
19	767.6	65.0	846	6	5164485-1 Sequence 5, Appl
20	767.2	65.0	6371	2	US-08-715-808-5 Sequence 12, Appl
21	767.2	65.0	6371	2	US-08-715-808-12 Sequence 14, Appl
22	764.8	64.8	3221	2	US-08-715-808-14 Sequence 14, Appl
23	764.8	64.8	3221	2	US-08-715-808-1 Sequence 9, Appl
24	756.4	64.0	846	4	US-09-247-890-9 Sequence 9, Appl
25	756.4	64.0	846	4	US-09-724-969-9 Sequence 9, Appl
26	756.4	64.0	846	4	US-09-724-852-9 Patent No. 5196194
27	756.2	64.0	3220	6	5196194-11 Patent No. 5196194

28	752.6	63.7	822	3	US-08-075-520A-14 Sequence 14, Appl
29	744.6	63.0	3215	2	US-09-719-528A-1 Sequence 1, Appl
30	731.8	62.0	893	4	US-08-500-914A-1 Sequence 1, Appl
31	693	58.7	5618	3	US-08-799-556-1 Sequence 1, Appl
32	693	58.7	5618	4	US-09-570-546-1 Sequence 1, Appl
33	672.4	56.9	801	4	US-09-311-784A-15 Sequence 15, Appl
34	652.2	55.2	681	5	PCT-US96-10602-13 Sequence 13, Appl
35	650.8	55.1	678	3	US-08-075-520A-26 Sequence 26, Appl
36	647.8	54.9	845	1	US-08-378-011A-2 Sequence 2, Appl
37	643.4	54.5	817	1	US-08-378-011A-4 Sequence 4, Appl
38	637	53.9	3504	2	US-08-760-797A-2 Sequence 2, Appl
39	637	53.9	3504	3	US-08-760-797A-4 Sequence 4, Appl
40	637	53.9	3504	3	US-08-932-929B-2 Sequence 2, Appl
41	637	53.9	3504	3	US-08-932-929B-4 Sequence 4, Appl
42	633	53.6	1194	5	PCT-US96-10602-5 Sequence 5, Appl
43	625	52.9	681	2	US-08-500-914A-7 Sequence 7, Appl
44	625	52.9	681	2	US-08-500-914A-9 Sequence 9, Appl
45	623.4	52.8	681	4	US-09-471-573A-1 Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-105-483-218
; Sequence 218, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-105-483-218

Query Match          94.6%; Score 1117.2; DB 1; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 ATGGGGCAGAACTCTTCACGACGACATCTCTGGAGTTCTTCCGACGACGAGTTGAT 60
|||||
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 QY 61 CCAGCCTTCAGAGCAACACCAACATCCAGATTGGGACTTCAATCCCAACAGAGACACC 120
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 QY 121 TGGCCAGAGCCCAACAGAGTAGAGCTGGAGCATTTGGGACTTGGGGTTTACCCCAACCCGAC 180
 Db 152 TGGCCAGAGCCCAACAGAGTAGAGCTGGAGCATTTGGGACTTGGGGTTTACCCCAACCCGAC 211
 QY 181 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCTTAACAAACACTTGGCCAGCAAT 240
 Db 212 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCTTAACAAACACTTGGCCAGCAAT 271
 QY 241 CCGCCTCTGCTTCCACCAATCGCCAGTCCAGGAAGAGCCCTACCCGCTGTCTCCACT 300
 Db 272 CCGCCTCTGCTTCCACCAATCGCCAGTCCAGGAAGAGCCCTACCCGCTGTCTCCACT 331
 QY 301 TTGAGAAACACTCATCTCAAGCCATGAGTGAATCCACAACTTTCCACAAACTCTG 360
 Db 332 TTGAGAAACACTCATCTCAAGCCATGAGTGAATCCACAACTTTCCACAAACTCTG 391
 QY 361 CAAGATCCAGAGTGAAGAGTCTGATTTCTCTGCTGTGCTCAAGTTGAGAGACGTA 420
 Db 392 CAAGATCCAGAGTGAAGAGTCTGATTTCTCTGCTGTGCTCAAGTTGAGAGACGTA 451
 QY 421 AACCTGTTCGAGTACTGCTCTCCATATGTCATATCTTCCAGAGATTGGGGACCT 480
 Db 452 AACCTGTTCGAGTACTGCTCTCCATATGTCATATCTTCCAGAGATTGGGGACCT 511
 QY 481 GCGGGAAACATGAGAAATCATCATCAGAGATTCTAGAGACCCCTGCTGTGTTACAGCG 540
 Db 512 GCGGTGAACATGAGAAATCATCATCAGAGATTCTAGAGACCCCTGCTGTGTTACAGCG 571
 QY 541 GGGTTTTCTTGTGACAAAGATCTCTCAATACCGAGAGTCTAGACTGTGTGACT 600
 Db 572 GGGTTTTCTTGTGACAAAGATCTCTCAATACCGAGAGTCTAGACTGTGTGACT 631
 QY 601 TCTCTCAATTTTCTAGGGGGAACACTACCGTGTCTTGGCCAAATTTGGAGTCCCAACC 660
 Db 632 TCTCTCAATTTTCTAGGGGGAACACTACCGTGTCTTGGCCAAATTTGGAGTCCCAACC 691
 QY 661 TCCATACTACCAACCTCTGCTCTCCAACTTGTCTGTGTTATCGCTGAGTGTCTG 720
 Db 692 TCCATACTACCAACCTCTGCTCTCCAACTTGTCTGTGTTATCGCTGAGTGTCTG 751
 QY 721 CGGGTTTTATCATCTTCTCTCTTATCTGCTGCTAGTCTGCTATCTTGTGTGTTCTT 780
 Db 752 CGGGTTTTATCATCTTCTCTCTTATCTGCTGCTAGTCTGCTATCTTGTGTGTTCTT 811
 QY 781 CTGAGACTACAAAGGATGTTGCGGTTTGTCTCTAATTTCCAGAGATCTTCAACACAGAC 840
 Db 812 CTGAGACTACAAAGGATGTTGCGGTTTGTCTCTAATTTCCAGAGATCTTCAACACAGAC 871
 QY 841 ACGGAGCATGAGAGCTGACAGCTCTGCTCAAGAAACCTTATGATCCCTCTCTGT 900
 Db 872 ACGGAGCATGAGAGCTGACAGCTCTGCTCAAGAAACCTTATGATCCCTCTCTGT 931
 QY 901 TGCCTGACAAAACCTTGGAGTGAAGACTGACCTGTATTCCTATCCCATCATCTCTGGAGCT 960
 Db 932 TGCCTGACAAAACCTTGGAGTGAAGACTGACCTGTATTCCTATCCCATCATCTCTGGAGCT 991
 QY 961 TTGGGAAATTTCTATGAGAGTGGAGCTCAGCCGTTTCTGAGCTCAGTTTATCTATGATG 1020
 Db 992 TTGGGAAATTTCTATGAGAGTGGAGCTCAGCCGTTTCTGAGCTCAGTTTATCTATGATG 1051
 QY 1021 CCATTTGTTAGTGTGTTGTAAGGCTTTCCCACTGTTTGGCTTTCAATTATATGATG 1080
 Db 1052 CCATTTGTTAGTGTGTTGTAAGGCTTTCCCACTGTTTGGCTTTCAATTATATGATG 1111
 QY 1081 ATGTTGTAAGTGGGGCCCAAGTCTGTACACATCTTGAAGTCCCTTTTAAACGCTGTATCA 1140
 Db 1112 ATGTTGTAAGTGGGGCCCAAGTCTGTACACATCTTGAAGTCCCTTTTAAACGCTGTATCA 1171

QY 1141 ATTTCTTTTGTCTTTGGTATACATTTAA 1170
 Db 1172 ATTTCTTTTGTCTTTGGTATACATTTAA 1201
 RESULT 2
 US-08-709-209-218
 ; Sequence 218, Application US/08709209
 ; Patent No. 5762938
 ; GENERAL INFORMATION:
 ; APPLICANT: Paolucci, Enzo
 ; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 ; TITLE OF INVENTION: STRAIN
 ; NUMBER OF SEQUENCES: 462
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis, Morris & Safford
 ; ADDRESSEE: c/o William S. Frommer
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/709, 209
 ; FILING DATE: 21-AUG-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/105,483
 ; FILING DATE: 12-AUG-1993
 ; APPLICATION NUMBER: US 07/847,951
 ; FILING DATE: 06-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frommer, William S.
 ; REGISTRATION NUMBER: 25,506
 ; REFERENCE/DOCKET NUMBER: 454310-2400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 840-3333
 ; TELEFAX: (212) 840-0712
 ; INFORMATION FOR SEQ ID NO: 218:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1201 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-709-209-218
 Query Match 94.6%; Score 1117.2; DB 1; Length 1201;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGGGGAGAAATCTTTCCACCAAGCAATCTCTGGGATTTCTTCCCGACCAAGTTGGAT 60
 Db 32 ATGGGGGAGAAATCTTTCCACCAAGCAATCTCTGGGATTTCTTCCCGACCAAGTTGGAT 91
 QY 61 CCAGCCTTCAGAGCAACACCAACATCCAGATTGGGACTTCAATCCCAACAGAGACACC 120
 Db 92 CCAGCCTTCAGAGCAACACCAAGCAATCCAGATTGGGACTTCAATCCCAACAGAGACACC 151
 QY 121 TGGCCAGAGCCCAACAGAGTAGAGCTGGAGCATTTGGGACTTGGGGTTTACCCCAACCCGAC 180
 Db 152 TGGCCAGAGCCCAACAGAGTAGAGCTGGAGCATTTGGGACTTGGGGTTTACCCCAACCCGAC 211
 QY 181 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCTTAACAAACACTTGGCCAGCAAT 240
 Db 212 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCTTAACAAACACTTGGCCAGCAAT 271
 QY 241 CCGCCTCTGCTTCCACCAATCGCCAGTCCAGGAAGAGCCCTACCCGCTGTCTCCACT 300

272 CCGCTCTGCTCCACCAATGCGCAGAGAGGACCTAACCCCGCTCTCCACCT 331
301 TTGAGAAACACTCATCTCTAAGCAGTGAAGTCCACAACTTCCACCAACTCTG 360
332 TTGAGAAACACTCATCTCTAAGCAGTGAAGTCCACAACTTCCACCAACTCTG 391
361 CAAGATCCCAAGTGAAGTCTGTATTTCCCTGCTGTGCTCCAGTTCAAGAACAGTA 420
392 CAAGATCCCAAGTGAAGTCTGTATTTCCCTGCTGTGCTCCAGTTCAAGAACAGTA 451
421 AACCTGTTCCGACTCTGTCTCTCCGATATGTCAATCTTCTCGAGATTTGGGACCT 480
452 AACCTGTTCCGACTCTGTCTCTCCGATATGTCAATCTTCTCGAGATTTGGGACCT 511
481 GCGCGAATGAGAAACATCATCAGAGATTCCTAGAACCCCTGCTCGTTACAGAGG 540
512 GCGCGAATGAGAAACATCATCAGAGATTCCTAGAACCCCTGCTCGTTACAGAGG 571
541 GCGGTTTCTTGTGAAGAAATCTCAGAAATACGAGATCTAGACTGTGTGAGCT 600
572 GCGTCTCTTGTGTGAAGAAATCTCAGAAATACGAGATCTAGACTGTGTGAGCT 631
601 TCTCTCAATTTCTTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCCCACT 660
632 TCTCTCAATTTCTTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCCCACT 691
661 TCCAAATGACTCAGCAACTCTGCTCCGATATGTCAATCTTCTCGAGATTTGGGACCT 720
692 TCCAAATGACTCAGCAACTCTGCTCCGATATGTCAATCTTCTCGAGATTTGGGACCT 751
721 CCGGCTTTTATCATCTTCTCTTCAATCTCTGCTGTATGCTCATCTTCTTGTGCTT 780
752 CCGGCTTTTATCATCTTCTCTTCAATCTCTGCTGTATGCTCATCTTCTTGTGCTT 811
781 CTGAGCTATCAAGATATGTTGCCGTTTCTCTTATTCAGAGATCTTCAACCACTG 840
812 CTGAGCTATCAAGATATGTTGCCGTTTCTCTTATTCAGAGATCTTCAACCACTG 871
841 ACGGAGCAATGAGAGGCTCGACGACTCTGCTCAAGAACTCTATGATCCCTCTCT 900
872 ACGGAGCAATGAGAGGCTCGACGACTCTGCTCAAGAACTCTATGATCCCTCTCT 931
901 TCTCTGACAAACCTTCTGAGTGAAGTCACTGTATTCCTATCCATCTCTGAGCT 960
932 TCTCTGACAAACCTTCTGAGTGAAGTCACTGTATTCCTATCCATCTCTGAGCT 991
961 TTGCGAAATTTCTTAGGGAGTGGGCTCAGCCGTTTCTCTGCTCAGTTTACTAGTG 1020
992 TTGCGAAATTTCTTAGGGAGTGGGCTCAGCCGTTTCTCTGCTCAGTTTACTAGTG 1051
1021 CCATTTGTCAGTGTGCTGAGGGCTTCCGCACTGTTGGCTTCTAGTATATGATG 1080
1052 CCATTTGTCAGTGTGCTGAGGGCTTCCGCACTGTTGGCTTCTAGTATATGATG 1111
1081 ATGTGTACTGAGGGGCAAGTCTGTACACCATCTGAGTCCCTTTTACCGCTTACCA 1140
1112 ATGTGTACTGAGGGGCAAGTCTGTACACCATCTGAGTCCCTTTTACCGCTTACCA 1171
1141 ATTTCTTTTGTCTTGGGTATACATTTAA 1170
1172 ATTTCTTTTGTCTTGGGTATACATTTAA 1201

RESULT 3

US-08-458-101-218
Sequence 218, Application US/08458101

GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkins, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James

APPLICANT: No. 5765959, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audomert, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-218
Query Match 94.6%; Score 1117.2; DB 1; Length 1201;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
1 ATGGGCGAAGATCTTCCACGACGATCTCTGGGATCTTCCGACCACTGAGT 60
2 ATGGGCGAAGATCTTCCACGACGATCTCTGGGATCTTCCGACCACTGAGT 91
61 CCAGCTTTCAGAGCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGAC 120
92 CCAGCTTTCAGAGCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGAC 151
121 TGGCCAGAGCCCAACAGAGTGAAGCTGAGACTTTCGACTGGGGTTACCCACCG 180
152 TGGCCAGAGCCCAACAGAGTGAAGCTGAGACTTTCGACTGGGGTTACCCACCG 211
181 GAGAGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCATTAACAAACCTTGCAGCA 240
212 GAGAGCTTTTGGGGTGAAGCCCTCAGGCTCAGGGCATTAACAAACCTTGCAGCA 271
241 CCGCTCTGCTTCCACCAATTCGCGATCAGAGAAAGCAGCTACCCGCTGTCCACT 300
272 CCGCTCTGCTTCCACCAATTCGCGATCAGAGAAAGCAGCTACCCGCTGTCCACT 331
301 TTGAGAAACACTCATCTCTAAGCAGTGAAGTCCACAACTTCCACCAACTCTG 360
332 TTGAGAAACACTCATCTCTAAGCAGTGAAGTCCACAACTTCCACCAACTCTG 391
361 CAAGATCCCAAGTGAAGTCTGTATTTCCCTGCTGTGCTCCAGTTCAAGAACAGTA 420

|||||
Db 392 CAAGATCCAGAGTGAAGAGCCTGTATTTCTCGTGTGGTCCAGTTCAGAGAGCAGTA 451
421 AACCCGTGTCGACTCTGTCTCTCCCATATGCGCATCTTTTCGAGAGATTGGGAGCCCT 480
452 AACCCGTGTCGACTCTGTCTCTCCCATATGCGCATCTTTTCGAGAGATTGGGAGCCCT 511
481 GCGCGAACAATGAGAAACATCAATCAGATTCCTAGAGACCCCTGCTCGTGTAAACAGCG 540
512 GCGCTGAACAATGAGAAACATCAATCAGATTCCTAGAGACCCCTGCTCGTGTAAACAGCG 571
541 GGGTTTTCTGTTGACAAATCTTCAATAACCGAGAGTCTAGACTCGTGTGAGACT 600
572 GGGTTCTTCTGTTGACAAATCTTCAATAACCGAGAGTCTAGACTCGTGTGAGACT 631
601 TCTCTCAATTTTCTAGGGGGAACACTACCGTGTCTTGGCCAAAATTGGCGATCCCAACC 660
632 TCTCTCAATTTTCTAGGGGGAACACTACCGTGTCTTGGCCAAAATTGGCGATCCCAACC 691
661 TCCAACTACTCAACCAACTCTGCTGCTCAACTGTCTGTTATCGTGGATGTGTCTG 720
692 TCCAACTACTCAACCAACTCTGCTGCTCAACTGTCTGTTATCGTGGATGTGTCTG 751
721 CGGCGTTTATCAATCTTCTCTTCTCATCTGCTGTATGCTCATCTTCTGTTGTTCTT 780
752 CGGCGTTTATCAATCTTCTCTTCTCATCTGCTGTATGCTCATCTTCTGTTGTTCTT 811
841 ACAGGACATGACAGAGCTGACAGACTCTGCTCAAGAAACCTGTATGTATCCCTCCTGT 900
872 ACAGGACATGACAGAGCTGACAGACTCTGCTCAAGAAACCTGTATGTATCCCTCCTGT 931
901 TGTGTACAAACCTTCCGATGGAATGCACTGTATTTCCATCCCATCATCTTGGGCT 960
932 TGTGTACAAACCTTCCGATGGAATGCACTGTATTTCCATCCCATCATCTTGGGCT 991
961 TTGGGAAATTTCTATGAGAGTGGGCTCAGCCCGTTTCTCCGAGCTCAAGTTAATGATG 1020
992 TTGGGAAATTTCTATGAGAGTGGGCTCAGCCCGTTTCTCCGAGCTCAAGTTAATGATG 1051
1021 CCATTTGTTCAAGTGTCTGTAGAGCTTTCCGCCACTGTTTGGCTTTCAGTTAATGATG 1080
1052 CCATTTGTTCAAGTGTCTGTAGAGCTTTCCGCCACTGTTTGGCTTTCAGTTAATGATG 1111
1081 ATGTTGTAAGTGGGGGCAAGTCTGTACACCAATCTTGAATCCCTTTTAAACCGCTGTACCA 1140
1112 ATGTTGTAAGTGGGGGCAAGTCTGTACACCAATCTTGAATCCCTTTTAAACCGCTGTACCA 1171
1141 ATTTTCTTTTGTCTTTGGGTATATCAATTAA 1170
1172 ATTTTCTTTTGTCTTTGGGTATATCAATTAA 1201

RESULT 4
US-08-105-483-215
; Sequence 215, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paoleletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-215

Query Match 94.6%; Score 1117.2; DB 1; Length 1285;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

1 ATGGGCGAGAAATCTTTCCACAGCAATCTCTGGGATTTCTTCCGACACACAGTTGGAT 60
116 ATGGGCGAGAAATCTTTCCACAGCAATCTCTGGGATTTCTTCCGACACACAGTTGGAT 135
61 CAGCCTTCAGACCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACACC 120
176 CAGCCTTCAGACCAACCAACCAATCCAGATTGGGACTTCAATCCCAAGAGACACC 235
121 TGCGCAGAGCCCAACAGATGAGAGCTGAGAGATTGGGCTTCAACCCCAACCGGAC 180
236 TGCGCAGAGCCCAACAGATGAGAGCTGAGAGATTGGGCTTCAACCCCAACCGGAC 235
181 GAGAGCCTTTTGGGGTGGAGCCCTCAGAGCTCAGGGCATTAACAACAACTTGGCCAGAAAT 240
296 GAGAGCCTTTTGGGGTGGAGCCCTCAGAGCTCAGGGCATTAACAACAACTTGGCCAGAAAT 355
241 CGGCTCTCTGCTTCCACCAATGCGCAGTCAAGAGGAGCTTACCCCGCTGTCTCAACT 300
356 CGGCTCTCTGCTTCCACCAATGCGCAGTCAAGAGGAGCTTACCCCGCTGTCTCAACT 415
301 TTGAGAAACATCATCTCTCAAGCATGAGTGAATCCCAACATTTTCCCAACAACTCTG 360
416 TTGAGAAACATCATCTCTCAAGCATGAGTGAATTTCCCAACATTTTCCCAACAACTCTG 475
361 CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGTGTGCTCCAGTTTCAAGAAACAGTA 420
476 CAAGATCCAGAGTGAAGGTCTGTATTTCCCTGCTGTGTGCTCCAGTTTCAAGAAACAGTA 535
421 AACCTGTTCGACTACTGTCTTCCCAATGCTCAATCTTCTCGAGAGATTGGGAGACCT 480
536 AACCTGTTCGACTACTGTCTTCCCAATGCTCAATCTTCTCGAGAGATTGGGAGACCT 595
481 GCGCGAACAATGAGAAACATCAATCAGATTCCTAGAGACCCCTGCTCGTGTAAACAGCG 540
596 GCGCTGAACAATGAGAAACATCAATCAGATTCCTAGAGACCCCTGCTCGTGTAAACAGCG 655
541 GGGTTTTCTGTTGACAAATCTTCAATAACCGAGAGTCTAGACTCGTGTGAGACT 600
656 GGGTTCTTCTGTTGACAAATCTTCAATAACCGAGAGTCTAGACTCGTGTGAGACT 715
601 TCTCTCAATTTTCTAGGGGGAACACTACCGTGTCTTGGCCAAAATTGGCGATCCCAACC 660

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Db 716 TCTCTCAATTTTCTAGGGGGAATACCGTGTCTTGGCCAAATTCGACGATCCCAACC 775
Qy 661 TCCATCACTACCAACCTCTGTCTTCCAACTTGTGATGATGATGATGATGATGATGATG 720
Db 776 TCCATCACTACCAACCTCTGTCTTCCAACTTGTGATGATGATGATGATGATGATGATG 835
Qy 721 CGGCGTTTATCATCTTCTCTTCACTGCTGCTATGCTATGCTATGCTATGCTATGCTATG 780
Db 836 CGGCGTTTATCATCTTCTCTTCACTGCTGCTATGCTATGCTATGCTATGCTATGCTATG 895
Qy 781 CTGACATCAAGATATGTTGCCGTTTGTCTCTTAATTCAGATCTTCAACCAACGAC 840
Db 896 CTGACATCAAGATATGTTGCCGTTTGTCTCTTAATTCAGATCTTCAACCAACGAC 955
Qy 841 ACGGACCATGAGAGCTGCAAGATCTGCTGCTCAAGGAACCTATGATCCCTCTGT 900
Db 956 ACGGACCATGAGAGCTGCAAGATCTGCTGCTCAAGGAACCTATGATCCCTCTGT 1015
Qy 901 TCTCTACAAAACCTTGGAGTGAACCTGACCTGTATTCACATCCATCATCTGAGCT 960
Db 1016 TCTCTACAAAACCTTGGAGTGAACCTGACCTGTATTCACATCCATCATCTGAGCT 1075
Qy 961 TTGCGAAATTCCTATGAGAGTGGGCTTACGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1076 TTGCGAAATTCCTATGAGAGTGGGCTTACGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 1135
Qy 1021 CCATTTGTTAGTGGTGTGAGAGCTTCCGCACTGTGCTTCACTGCTGCTGCTGCTGCTG 1080
Db 1136 CCATTTGTTAGTGGTGTGAGAGCTTCCGCACTGTGCTTCACTGCTGCTGCTGCTGCTGCT 1195
Qy 1081 ATGTTGATCTGGGAGCAAGTCTGTAACAACATCTGAGTCCCTTTTACCGCTGTTACCA 1140
Db 1196 ATGTTGATCTGGGAGCAAGTCTGTAACAACATCTGAGTCCCTTTTACCGCTGTTACCA 1255
Qy 1141 ATTTCTTTTGTCTTGTGGTATACATTAA 1170
Db 1256 ATTTCTTTTGTCTTGTGGTATACATTAA 1285

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RESULT 5

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US-08-709-209-215
; Sequence 215, Application US/08709209
; Patent No. 5762938
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,209
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506

```

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; REFERENCE/DOCKET NUMBER: 454310-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-709-209-215
Query Match 94.6%; Score 1117.2; DB 1; Length 1285;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Db 956 ACCGACCATGCCGAACTCATCTACTGCTCAAGAACTCTATGATCCCTCTGT 1015
Qy 901 TGCTGTACAAACCTTGATGAGAACTGACACCTGTATCCCATCCATATCTGGGCT 960
Db 1016 TGCTGTACAAACCTTGAGAGGAAATGGACCTGTATCCCATCCATATCTGGGCT 1075
Qy 961 TTGGAAATTCCTATGAGAGTGGGCTCAAGCCGTTCTCTGGCTCAGTTTACTAGT 1020
Db 1076 TTGGAAATTCCTATGAGAGTGGGCTCAAGCCGTTCTCTGGCTCAGTTTACTAGT 1135
Qy 1021 CCATTTGTAGAGTGTCTGAGAGCTTCCGCCCTGTTGGCTTCAATTATATGATG 1080
Db 1136 CCATTTGTAGAGTGTCTGAGAGCTTCCGCCCTGTTGGCTTCAATTATATGATG 1195
Qy 1081 ATGTGTATGGGGGCCAAGCTGTATACCACTGTGAGTCCCTTTTACCGGTTACCA 1140
Db 1196 ATGTGTATGGGGGCCAAGCTGTATACCACTGTGAGTCCCTTTTACCGGTTACCA 1255
Qy 1141 ATTTCTTTTGTCTTTGGGTATACATTTAA 1170
Db 1256 ATTTCTTTTGTCTTTGGGTATACATTTAA 1285

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RESULT 6

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US-08-458-101-215
; Sequence 215, Application US/08458101
; Patent No. 5765599

```

GENERAL INFORMATION:

```

; APPLICANT: Pacietti, Enzo
; APPLICANT: Perkins, Marion E.
; APPLICANT: Taylor, Jill
; APPLICANT: Tartaglia, James
; APPLICANT: No. 576599ton, Elizabeth K.
; APPLICANT: Riviere, Michel
; APPLICANT: de Taine, Charles
; APPLICANT: Limbach, Keith J.
; APPLICANT: Johnson, Gerard P.
; APPLICANT: Pincus, Steven E.
; APPLICANT: Cox, William I.
; APPLICANT: Audonnet, Jean-Christophe Francis
; APPLICANT: Gettig, Russell Robert
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,101
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 base pairs
; TYPE: nucleic acid

```

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; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-458-101-215
Query Match 94.6%; Score 1117.2; DB 1; Length 1285;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 ATGGGCGAGATCTTTTCCACAGCAATCTCTGGGATCTTTTCCGACACAGTGGAT 60
Db 116 ATGGGCGAGATCTTTTCCACAGCAATCTCTGGGATCTTTTCCGACACAGTGGAT 175
Qy 61 CCAGCTTCAGAGCAAAACCAAAATCCAGATTGGAGCTTCAATCCCAAGAGACCC 120
Db 176 CCAGCTTCAGAGCAAAACCAAAATCCAGATTGGAGCTTCAATCCCAAGAGACCC 235
Qy 121 TTGGCCAGAGCCCAACAAAGTAGAGGTGGAGCATTTGGAGTTCACCCACCGCAC 180
Db 236 TTGGCCAGAGCCCAACAAAGTAGAGGTGGAGCATTTGGAGTTCACCCACCGCAC 295
Qy 181 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACCTTGGCAGCAAT 240
Db 296 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACCTTGGCAGCAAT 355
Qy 241 CGGCTTCTGCTTCCACCAATGCGCAGTAGAGAGCGCTTACCCGCTGTCTCCACT 300
Db 356 CGGCTTCTGCTTCCACCAATGCGCAGTAGAGAGCGCTTACCCGCTGTCTCCACT 415
Qy 301 TTGAGAAACATCATCTCTCAAGCATGAGTGGAACTTCCACCACTTCCACCAACTCT 360
Db 416 TTGAGAAACATCATCTCTCAAGCATGAGTGGAACTTCCACCACTTCCACCAACTCT 475
Qy 361 CAAGATCCAGAGTGGAGGTCTGTATTTCCCTGTGTGTGCTTCAAGTTCAGAGCAAGTA 420
Db 476 CAAGATCCAGAGTGGAGGTCTGTATTTCCCTGTGTGTGCTTCAAGTTCAGAGCAAGTA 535
Qy 421 AACCTGTTCGACATCTGTCTTCCCATATCTCTCAATCTTCTGAGAGATTGGGACCT 480
Db 536 AACCTGTTCGACATCTGTCTTCCCATATCTCTCAATCTTCTGAGAGATTGGGACCT 595
Qy 481 GCGGGAACATGGAGAAACATCATAGAGATTCTTGGGACCCCTGCGGTGTTACAGGGC 540
Db 596 GCGGGAACATGGAGAAACATCATAGAGATTCTTGGGACCCCTGCGGTGTTACAGGGC 655
Qy 541 GGGTTTTTCTTGTGCAAGAACTCTCAATATCCGACAGTCTAGACTGTGTGAGT 600
Db 656 GGGTTTTTCTTGTGCAAGAACTCTCAATATCCGACAGTCTAGACTGTGTGAGT 715
Qy 601 TCTCTCAATTTTCTAGGGGAACTACCGTGTGTCTTGGCCAAATTCGAGTCCCAACC 660
Db 716 TCTCTCAATTTTCTAGGGGAACTACCGTGTGTCTTGGCCAAATTCGAGTCCCAACC 775
Qy 661 TTCAATCATCACCACCTCTGTCCCTCAACTGTCTGGTATATGGCTGGATGTGTCT 720
Db 776 TTCAATCATCACCACCTCTGTCCCTCAACTGTCTGGTATATGGCTGGATGTGTCT 835
Qy 721 CGGCGTTTATCATCTTCTCTTCACTGCTGCTATATGCTCATCTTCTTGTGTCTT 780
Db 836 CGGCGTTTATCATCTTCTCTTCACTGCTGCTATATGCTCATCTTCTTGTGTCTT 895
Qy 781 CTGAGACTATCAAGATATGTTGCCGTTTGTCTCTTATATTCAGAGATCTTCAACACAGC 840
Db 896 CTGAGACTATCAAGATATGTTGCCGTTTGTCTCTTATATTCAGAGATCTTCAACACAGC 955
Qy 841 ACCGACCATGACAGCTGCTGACAGCTCTGCTCAAGGAACCTTATATGATCCCTCTGT 900
Db 956 ACCGACCATGACAGCTGCTGACAGCTCTGCTCAAGGAACCTTATATGATCCCTCTGT 1015
Qy 901 TGCTGTACAAACCTTGATGAGAACTGACACCTGTATCCCATCCATATCTGGGCT 960
Db 1016 TGCTGTACAAACCTTGAGAGGAAATGGACCTGTATCCCATCCATATCTGGGCT 1075
Qy 961 TTGGAAATTCCTATGAGAGTGGGCTCAAGCCGTTTCTCTGGCTCAGTTTACTAGT 1020

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Db 1076 TTGGAAAAATTCCTATGAGGAGTGAGGCTCAGCCCGTTCTCCGTGAGCTCAGTTACTAGTG 1135
Qy 1021 CCATTGTCAGTGGTTCGTAGGCTTTCCCCACATGTTGGCTTCACTTATATGATG 1080
Db 1136 CCATTGTCAGTGGTTCGTAGGCTTTCCCCACATGTTGGCTTCACTTATATGATG 1195
Qy 1081 ATGTTGTAAGGAGGCAAGTCTGTACACATCTTGAAGTCCCTTTTACCGCTGTACCA 1140
Db 1196 ATGTGTAATTTGGGGGCAAGTCTGTACACATCTTGAAGTCCCTTTTACCGCTGTACCA 1255
Qy 1141 ATTTCTTTTGTCTTTGGGTATACATTAA 1170
Db 1256 ATTTCTTTTGTCTTTGGGTATACATTAA 1285
RESULT 7
US-08-480-173A-42
; Sequence 42, Application US/08480173A
; Patent No. 6072049
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans A
; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Popovich & Miles, P.A.
; STREET: 80 S. 8th Street, Suite 1902
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,173A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Popovich, Thomas E
; REGISTRATION NUMBER: 30,099
; REFERENCE/DOCKET NUMBER: MED1003USD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-334-8991
; TELEFAX: 612-334-8994
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 12..14
; OTHER INFORMATION: /note="S1 start codon"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 336..338
; OTHER INFORMATION: /note="S2 start codon"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 508..510
; OTHER INFORMATION: /note="S start codon"
US-08-480-173A-42
Query Match 92.1%; Score 1088.2; DB 3; Length 2348;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 33; Indels 9; Gaps 3;
Qy 1 ATGGGAGCAAAATCTTCCACGCAATCCTCTGAGTCTTCCGACGACGAGTTGAT 60

Db 12 ATGGGAGCAAAATCTTCCACGCAATCCTCTGAGTCTTCCGACGACGAGTTGAT 71
Qy 61 CCAAGCTTCAGAGCAAAACCAACAATCCAGATTGGACCTTAAATCCCAAGAGACAC 120
Db 72 CCAAGCTTCAGAGCAAAACCAACAATCCAGATTGGACCTTAAATCCCAAGAGACAC 131
Qy 121 TGGCCAGAGCGCCAAAGATAGAGCTGAGAGATTCCGACTGGGGGTTCACCCACGAC 180
Db 132 TGGCCAGAGCGCCAAAGATAGAGCTGAGAGATTCCGACTGGGGGTTCACCCACGAC 191
Qy 181 GAGAGCCTTTTGGGGTGAAGCCCTCAGGCTCAAGGCAATACCAAACTTGGCAGCAAT 240
Db 192 GAGAGCCTTTTGGGGTGAAGCCCTCAGGCTCAAGGCAATACCAAACTTGGCAGCAAT 251
Qy 241 CGGCTCTGCTTCCACCAATGCGCATGAGAGAGGCAAGCTTACCCGCTGTCCACT 300
Db 252 CGGCTCTGCTTCCACCAATGCGCATGAGAGAGGCAAGCTTACCCGCTGTCCACT 311
Qy 301 TTGAGAAACATCATCTCAAGCCATGAGAGTGAAGTCCCAAACTTTCACCAACTCG 360
Db 312 TTGAGAAACATCATCTCAAGCCATGAGAGTGAAGTTCACCAACTTTCACCAACTCG 371
Qy 361 CAAGATCCAGAGTGAAGGCTGTATTTCCCTGCTGGTGCT-----CCAGTTTCAG 413
Db 372 CAAGATCCAGAGTGAAGGCTGTATTTCCCTGCTGGTGCTCCAGTTCCCAAGTTTCAG 431
Qy 414 AACAGTAAACCTGTTCCGACTACTGTCTTCCCATATGCTCATCTTTCGAGATTGG 473
Db 432 AACAGTAAACCTGTTCCGACTACTGTCTTCCCATATGCTCATCTTTCGAGATTGG 491
Qy 474 GGACCTCGGCGGAGATGAGAGACATCATCAGATTTCTTGAAGACCCCTGCTGTGT 533
Db 492 GGACCTCGGCGGAGATGAGAGACATCATCAGATTTCTTGAAGACCCCTGCTGTGT 551
Qy 534 ACAGGCGGGGGTCTTCTTGTGACAAAGATCTCAAAATACCGCAGAGTCTAGACTCGT 593
Db 552 ACAGGCGGGGGTCTTCTTGTGACAAAGATCTCAAAATACCGCAGAGTCTAGACTCGT 610
Qy 594 GTGACTTCTCTCAATTTTCTAGGGGGAATACCTGCTGTCTTGGCCAAATTCGCAATC 653
Db 611 GTGACTTCTCTCAATTTTCTAGGGGGAATACCTGCTGTCTTGGCCAAATTCGCAATC 670
Qy 654 CCAACCTCCATCACTACCAACCTCCGTCCTCAACTGTCTGCTGATATCGGTGAT 713
Db 671 CCAACCTCCATCACTACCAACCTCCGTCCTCAACTGTCTGCTGATATCGGTGAT 730
Qy 714 GTGCTGGGGGCTTTATCATCTTCTCTTCACTGCTGATATCGGTGATATCGGTGAT 773
Db 731 GTGCTGGGGGCTTTATCATCTTCTCTTCACTGCTGATATCGGTGATATCGGTGAT 790
Qy 774 GGTCTTTCGACATATCAAGGTATGTGCCGCTTGTCTCTAATTCAGAGATCTTCAAC 833
Db 791 GGTCTTTCGACATATCAAGGTATGTGCCGCTTGTCTCTAATTCAGAGATCTTCAAC 850
Qy 834 CACGAGCAAGGAGCATGAGAGCTGACAGCTCTCTCAAGTCTCTCAAGAACCTCATATCC 893
Db 851 AACGAGCAAGGAGCATGAGAGCTGACAGCTCTCTCAAGTCTCTCAAGAACCTCATATCC 910
Qy 894 CTCCTGTTGCTGTACAAACCTTCGATGAGAACTGACACTGATATCCCATCATATC 953
Db 911 CTCCTGTTGCTGTACAAACCTTCGATGAGAACTGACACTGATATCCCATCATATC 970
Qy 954 CTGGGCTTTCGAAATTCCTATAGGAGTGGGCTCAGCCGCTTCTCTGAGTCAAGTTT 1013
Db 971 CTGGGCTTTCGAAATTCCTATAGGAGTGGGCTCAGCCGCTTCTCTGAGTCAAGTTT 1030
Qy 1014 ACTAGTGCATTTGTTGAGTGTGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCAGTAT 1073
Db 1031 ACTAGTGCATTTGTTGAGTGTGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGTAT 1090
Qy 1074 ATGATGATGTTGTACTGGGGGCAAGTCTG-TACACCATCTTGAATCCCTTTTACCGC 1132

Db 1091 ATGATGATGTGTATTTGGGGGCCCAAGCTCTGTACACATCTTGATCCCTTTTAAACCC 1150
Qy 1133 TGTACCAATTTTCTTTGTCTTTGGGTATACATTTAAACCTTAATAA 1181
Db 1151 TGTACCAATTTTCTTTGTCTTTGGGTATACATTTAAACCTTAACAA 1199

RESULT 8

US-08-484-408A-42
; Sequence 42, Application US/08484408A
; Patent No. 6117653
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans A
; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Popovich & Wiles, P.A.
; STREET: 80 S. 8th Street, Suite 1902
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,408A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Popovich, Thomas E
; REGISTRATION NUMBER: 30,099
; REFERENCE/DOCKET NUMBER: MED1003USD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-334-8991
; TELEFAX: 612-334-8994
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 12..14
; OTHER INFORMATION: /note= "S1 start codon"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 336..338
; OTHER INFORMATION: /note= "S2 start codon"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 508..510
; OTHER INFORMATION: /note= "S start codon"
US-08-484-408A-42

Query Match 92.1%; Score 1088.2; DB 3; Length 2348;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 33; Indels 9; Gaps 3;

Qy 1 ATGGGGGAGAACTTTCCACAGCAATCTCTGGGATTTCCCGACCAACAGTGGAT 60
Db 12 ATGGGGGAGAACTTTCCACAGCAATCTCTGGGATTTCCCGACCAACAGTGGAT 71
Qy 61 CCAAGCTTTCAGAGCAACCAACCAATTCAGATTGGACTTCATCCCAACAGAGACC 120
Db 72 CCAAGCTTTCAGAGCAACCAACCAATTCAGATTGGACTTCATCCCAACAGAGACC 131
Qy 121 TGGCAGACGCGCAACAAAGTAGAGCTGGAGCAATTCGAGCTGGGGTTCAACCCACCGCAC 180

Db 132 TGGCCAGACGCCAACAAAGGTAGAGCTGAGCAATTCGGCTGGGTTTCAACCCACCGCAC 191
Qy 181 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGGATTAACAAACCTTGGCCAGCAAT 240
Db 192 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGGATTAACAAACCTTGGCCAGCAAT 251
Qy 241 CCGCTCTCTGCTTTCACCAATCGCAGTCAAGAAAGGACCTTACCCGCTGTCTCACT 300
Db 252 CCGCTCTCTGCTTTCACCAATCGCAGTCAAGAAAGGACCTTACCCGCTGTCTCACT 311
Qy 301 TTGAGAAACATCATCTCTCAAGCATGACGTGAATCTCCACAACTTTCCACCAACTCG 360
Db 312 TTGAGAAACATCATCTCTCAAGCATGACGTGAATCTCCACAACTTTCCACCAACTCG 371
Qy 361 CAAGATCCAGAGTGAAGGTCTGTAATTCCTCGCTGAGTGGCT-----CCAGTTCAAG 413
Db 372 CAAGATCCAGAGTGAAGGTCTGTAATTCCTCGCTGAGTGGCT-----CCAGTTCAAG 431
Qy 414 AACAGTAAACCTCTTCCGACTATCTCTCTCCATATCTGCAATCTTCTGAGATTGG 473
Db 432 AACAGTAAACCTCTTCTGACTACTCTCTCTCTATCGTCAATCTTCTGAGATTGG 491
Qy 474 GGAACCTCGCGGGAATGAGAAATCATCATAGAGATTCCTAGAACCCCTGCTCGTGT 533
Db 492 GGAACCTCGCGTGAATGAGAAATCATCATAGAGATTCCTAGAACCCCTGCTCGTGT 551
Qy 534 ACAGGCGGGGTTTTCTGTGACAAAGAACTCTCAATACGSCAGAGTCTAGACTCGT 593
Db 552 ACAGGCGGGGTTTTCTGTGACAAAGAACTCTCAATACGSCAGAGTCTAGACTCGT 610
Qy 594 GTGACTTCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCC 653
Db 611 GTGACTTCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCC 670
Qy 654 CCCAAGCTTCAATCACTCAACCAACCTCTCTCTCCAACTTGTCTGTTATGCGTGGAT 713
Db 671 CCCAAGCTTCAATCACTCAACCAACCTCTCTCTCCAACTTGTCTGTTATGCGTGGAT 730
Qy 714 GTGCTGCGGCGTTTTATCATCTTCTCTTCACTCTGCTGATGCTCATCTTCTGTT 773
Db 731 GTGCTGCGGCGTTTTATCATCTTCTCTTCACTCTGCTGATGCTCATCTTCTGTT 790
Qy 774 GGTCTTCTGAGACTATCAAGTATGTGCGCGTTTGTCTTAATTCAGAGATCTTCAAC 833
Db 791 GGTCTTCTGAGACTATCAAGTATGTGCGCGTTTGTCTTAATTCAGAGATCTTCAAC 850
Qy 834 CACGAGCAGGAGCAATGACAGACCTGACAGATCTCTGCTCAAGAACTCTATATGATCC 893
Db 851 AACGAGCAGGAGCAATGACAGACCTGACAGATCTCTGCTCAAGAACTCTATATGATCC 910
Qy 894 CTCCTGTGTGTACAAAACTTCCGATGGAACCTGACCTGATTCCTATCCATCCATCATC 953
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Qy 954 CTGGGCTTTGGAAAAATCTCTATGGAAGTGGGCTCAGCCGTTTCTCTGCTCAGTTT 1013
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Qy 1014 ACTAGTGCATTTGTTTCAGTGTCTGTAAGGCTTTCCCACTGTTTGGCTTTCAGTTAT 1073
Db 1031 ACTAGTGCATTTGTTTCAGTGTCTGTAAGGCTTTCCCACTGTTTGGCTTTCAGTTAT 1090
Qy 1074 ATGATGATGTGTACTGGGGGCAAGTCTG-TACACATCTTGAGTCCCTTTTACCGC 1132
Db 1091 ATGATGATGTGTATTTGGGGGCAAGTCTGTTTACAGATCTTGAGTCCCTTTTACCGC 1150
Qy 1133 TGTACCAATTTTCTTTGTCTTTGGGTATACATTTAAACCTTAATAA 1181
Db 1151 TGTACCAATTTTCTTTGTCTTTGGGTATACATTTAAACCTTAACAA 1199

RESULT 9

US-08-854-531-5

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Sequence 5, Application US/08854531
Patent No. 6025341
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Tokushige, Katsutoshi
APPLICANT: Wakita, Takaji
TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6025341r1s
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,531
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOI-0214
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-854-531-5

Query Match      84.7%; Score 1000.6; DB 3; Length 1200;
Best Local Similarity 91.1%; Pred. No. 1,8e-294;
Matches 1063; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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454 AACCTGTTCCGACTACTGTCTCACCATATGTCATCTCTCGAGAGACTGGGACCGT 513
481 GCGCGGACATGAGAGACATCATCAGGATTCTAGAGACCCCTGCTGTTACAGGGG 540
514 GCACGACATGAGAGACATCAGATGAGATTCAGAGACCCCTGCTGTTACAGGGG 573
541 GGGTTTTCTTTGTCAGAGAAATCTCAGATACGAGAGTCTAGTCTGTTGAGT 600
574 GGGTTTTCTTTGTCAGAGAAATCTCAGATACGAGAGTCTAGTCTGTTGAGT 633
601 TCTCTCAATTTCTAGGGGAACTACCGTGTCTTGGCCAAATTCGAGTCCCAAC 660
634 TCTCTCAATTTCTAGGGGAGACACCGATGTCTGCGCAAAATTCGAGTCCCAAC 693
661 TCCATACATCCACACCTCTGCTCCAACTTGCTCGTTATTCGATGATGTCTG 720
694 TCCATACATCCACACCTCTGCTCCAACTTGCTCGTTATTCGATGATGTCTG 753
721 CCGCGTTTATCATCTCTCTTCATCTGCTGATAGCTCATCTCTTGTGTTCTT 780
754 CCGCGTTTATCATCTCTCTTCATCTGCTGATAGCTCATCTCTTGTGTTCTT 813
781 CTGACTATCAAGTATGTGCGCTTGCTGCTTAATTCAGATCTTCAACACACGAC 840
814 CTGACTATCAAGTATGTGCGCTTGCTGCTTAATTCAGATCTTCAACACACGAC 873
841 ACAGGACCATGAGACCTGACAGCTCTGCTCAAGGAACTCTATGATCCCTCTCT 900
874 ACAGGACCATGAGACCTGACAGCTCTGCTCAAGGAACTCTATGATCCCTCTCT 933
901 TCTGTACAAACCTTCGATGAGAACTGACCTGATTCGATCCGATCATCTGAGGCT 960
934 TCTGTACAAACCTTCGATGAGAACTGACCTGATTCGATCCGATCATCTGAGGCT 993
961 TTGGAATAATCTATGAGAGTGGGCTTCAGCCGCTTCTCTGCTCAGTTACTAGT 1020
994 TTGGAATAATCTATGAGAGTGGGCTTCAGCCGCTTCTCTGCTCAGTTACTAGT 1053
1021 CCATTTGTCATGCTGTCTAGGCTTTCCGCCATCTGTTGCTTCACTATAGAGT 1080
1054 CCATTTGTCATGCTGTCTAGGCTTTCCGCCATCTGTTGCTTCACTATAGAGT 1113
1081 ATGTGTACTGGGGGCAAGCTGTACACCATCTGAGTCCCTTTTACCGCTTACCA 1140
1114 ATGTGTACTGGGGGCAAGCTGTACACCATCTGAGTCCCTTTTACTTACTATACCA 1173
1141 ATTTCTTTTGTCTTGGGTATACAT 1167
1174 ATTTCTTTTGTCTTGGGTATACAT 1200

RESULT 10
PCT-US95-13552-5
Sequence 5, Application PC/TUS9513552
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Tokushige, Katsutoshi
APPLICANT: Wakita, Takaji
APPLICANT: Pachuk, Catherine J.
APPLICANT: Zurawski, Jr., Vincent R.
APPLICANT: Coney, Leslie R.
TITLE OF INVENTION: HEPATITIS VIRUS VACCINES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13552
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,248
FILING DATE: 05-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,859
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL-0238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
PCT-US95-13552-5

Query Match 84.7%; Score 1000.6; DB 5; Length 1200;
Best Local Similarity 91.1%; Pred. No. 1.8e-294;
Matches 1063; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 ATGGGGAGATCTTTCCAGCAATCTCTGGGATTTCCCGACCAACCAATTGAT 60
DB 34 ATGGGGAGATCTTTCTGTTCCCAATCTCTGGGATTTCCCGACCAACCAATTGAT 93
QY 61 CCAAGCTTTCAGAGCAACCAACCAATTCAGATTGGGACTTCAATCCCAACAGACACC 120
DB 94 CTGCGCTTCGAGGCAACTCAACCAATTCAGATTGGGACTTCAATCCCAACAGACACC 153
QY 121 TGCCAGACGCCCAACAGATGAGCTGAGCAATTCGGATCGGGTTTACCCACCGCAC 180
DB 154 TGCCAGAGGAAATCAAGTGTAGAGCGGAGACTTCGGGTCAGGGTTTACCCACCGCAC 213
QY 181 GGAGGCTTTGGGGTGAAGCCCTCAGGCTCAGGGCAATACACAACTTCCGCAAT 240
DB 214 GGCGGCTTTGGGGTGAAGCCCTCAGGCTCAGGGCAATACACAACTTCCGCAAT 273
QY 241 CCGGCTCTGCTTCCACCAATCGCAGTCAAGAGGAGCCTACCCGCTGTCCACT 300
DB 274 CTTCTCTGCTCTCCACCAATCGGAGTCAAGAGGAGCCTACCTTCCACTTCTCCACT 333
QY 301 TTGAGAAACTCATCTCTCAAGCCATGAGTGAATTCACAACTTTCACCAAACTCTG 360
DB 334 CTAGAGACAGATCATCTCTCAGGCGCATGAGTGAATTCACAACTTTCACCAAACTCTG 393
QY 361 CAAGATCCAGAGTGAAGGTCTGATTTCCCTGCTGTGCTCCAGTTCAGAAAGTA 420
DB 394 CTAGATCCAGAGTGAAGGTCTGATTTCCCTGCTGTGCTCCAGTTCAGAAAGTA 453
QY 421 AACCTGTTCGAGTCACTGTCTCCATATGTCATCTTCTGAGGATTTGGGAGCCCT 480
DB 454 AACCTGTTCGAGTCACTGTCTCCATATGTCATCTTCTGAGGATTTGGGAGCCCT 513
QY 481 GCGGGAACATGAGAAATCATCATCAGATTTCTAGAGCCCTGCTGTGTTCAGAGCG 540
DB 514 GCACCGAATGAGAGAGCAACATCAGGATTTCTAGAGCCCTGCTGTGTTCAGAGCG 573
QY 541 GGGTTTTTCTTGTGACAAAGATCTCTCAATATCCGAGAGTCTAGAGTCTGTGTGACT 600
DB 574 GGGTTTTTCTTGTGACAAAGATCTCTCAATATCCGAGAGTCTAGAGTCTGTGTGACT 633

QY 601 TCTCTCAATTTCTAGGGGAACTACCGTGTGTTGGCCAAATTCGAGTCCCAACC 660
DB 634 TCTCTCAATTTCTAGGGGAACTACCGTGTGTTGGCCAAATTCGAGTCCCAACC 693
QY 661 TCCATATCATCACCACCTCTCTCTCTCAATTTGCTGTGTATAGTGTGTGTCTG 720
DB 694 TCCATATCATCACCACCTCTCTCTCTCAATTTGCTGTGTATAGTGTGTGTCTG 753
QY 721 CCGCGTTTATCATCT 780
DB 754 CCGCGTTTATCATCT 813
QY 781 CTGAGATATCAGATATGTTGCCGTTTGTCTCTAATTCAGAGATCTTCAACACAGC 840
DB 814 CTGAGATATCAGATATGTTGCCGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 873
QY 841 ACGGAGCATGAGAGCTCTGACAGCTCTGCTCTCAAGAACTCTATATATCTCTCTCT 900
DB 874 ACGGAGCATGAGAGCTCTGACAGCTCTGCTCTCAAGAACTCTATATGTTTCCCTCT 933
QY 901 TGCCTATCAAAACCTTCGATGAGAACTGACCTGTATTCATCCATCATCTCTGAGCT 960
DB 934 TGCCTATCAAAACCTTCGATGAGAACTGACCTGTATTCATCCATCATCTCTGAGCT 993
QY 961 TTGGAAAATTCCTATGAGAGTGGGCTCAGCCGTTTCTCTGCTCACTTACTAGTG 1020
DB 994 TTGCAAGATTCCTATGAGAGTGGGCTCAGCTCGTTTCTCTGCTCACTTACTAGTG 1053
QY 1021 CCAATTGTTCAAGTGTTCGAGGCTTTCCCACTGTTGGCTTCACTTATATAGTGT 1080
DB 1054 CCAATTGTTCAAGTGTTCGAGGCTTTCCCACTGTTGGCTTCACTTATATAGTGT 1113
QY 1081 ATGTTGACTGGGGGCAAGTCTGTACACCATCTTGAGTCTTTTACCGCTGTTACCA 1140
DB 1114 ATGTTGACTGGGGGCAAGTCTGTACACCATCTTGAGTCTTTTACCGCTGTTACCA 1173
QY 1141 ATTTCTTTTGTCTTTGGTATACAT 1167
DB 1174 ATTTCTTTTGTCTTTGGTATACAT 1200

RESULT 11
US-08-715-808-2
Sequence 2, Application US/08715808
Patent No. 5981274
GENERAL INFORMATION:
APPLICANT: Tyrrell, D. Lorne J.
APPLICANT: Chaisomchit, Sumonta
TITLE OF INVENTION: Recombinant Hepatitis Virus Vectors
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,808
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02441
TELECOMMUNICATION INFORMATION:


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: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9325 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "DNA"
US-08-715-808-2

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Query Match Similarity		84.7%	Score 1000.2	DB 2	Length 9325	
Query Local Similarity		90.4%	Pred. No. 6.5e-294			
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DB	3135	ATGGGGAGAAATCTTTCTGTTCCTCATCTCTGGATTTCTTCCGATCATCATGTTGGAC	3194			
QY	61	CCAGCTTTCAGAGCAAAACCAACATTCAGATTGGACATTCAATCCAAAGACAC	120			
DB	3195	CCTGATTTCCGAGCCCACTCAAAACATCCAGATTGGGACTTCAACCCCGTCAGAGACAC	3254			
QY	121	TGGCCAGACGCCAACAAGTAGSACTGAGATTCGATTCGATCGGGTTTCACCCCACCGAC	180			
DB	3255	TGGCCAGACGCCAACAAGTAGAATGGAGATTCGGAGCCCAAGGCTCAACCTTCACAC	3314			
QY	181	GGAGGCTTTTGGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAACAACCTTGCAGAGAA	240			
DB	3315	GGCGGTAATTTTGGGGTGAAGCCCTCAGGCTCAGGGCAATTTGACACACAGTGTCAACAA	3374			
QY	241	CCGCTCTCTGTTCCACCAATGCCAGTTCAGGAGGACGACCTTACCCCGCTGTCCACCT	300			
DB	3375	CCTCTCTCTGCTCCACCAATGGGACAGTTCAGGAGGACGACCTTACCTCTCTCACCT	3433			
QY	301	TTGGAACAACATCAATCTTCAGGCTCAGATGAGTAACTCCACAACCTTTCCACCAACTCTG	360			
DB	3435	CTAAGAGACAGTCAATCTTCAGGCTCAGATGAGTAAATCCACATGCTTCCACCAACTCTG	3494			
QY	361	CAAGATCCCAAGATGAGAGTCTGATTTTCCCTGCTGGGGTCCAGTTCAGAAACAGTA	420			
DB	3495	CAGATCCCAAGATGAGGGGTCTGATTTCTTCTGCTGGGGTCCAGTTCAGAAACAGTA	3554			
QY	421	AACCTGTTCGAGTACTGTCTCTCCATATGTCATTTTTCGAGATTGGGAGCCCT	480			
DB	3555	AACCTGTCTCGAATATTTGCTCTCAATCTGTCAATCTCGGAGGAGCTGGGAGCCCT	3614			
QY	481	GCGCGAAACATGAGAACATCATCATCAGGATCTTAGAGACCCCTGCTGTTACAGGGC	540			
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QY	541	GGGTTTTCTGTGACAAAGATCTCTCAATAACGAGAGTCTAGACTCGGTGGAGCT	600			
DB	3675	GGGTTTTCTGTGTACAAAGATCTCTCAATAACGAGAGTCTAGACTCGGTGGAGCT	3734			
QY	601	TCTCTCAATTTTCTAGGGGAACTACCGTGTCTTGTGCGAAATTCGAGTCCCAAC	660			
DB	3735	TCTCTCAATTTTCTAGGGGGAATCTCCGCTGTCTTGTGCGAAATTCGAGTCCCAAC	3794			
QY	661	TCCATCACTCAACCACTCTGTCTTCCAACTGTCTGTGTTATCGGTGATGTGTCTG	720			
DB	3795	TCCATCACTCAACCACTCTGTCTTCCAACTGTCTGTGTTATCGGTGATGTGTCTG	3854			
QY	721	CGGGTTTATCATCTTCTCTTAATCCGCTGCTATAGCTCATCTTCTTATTTGGTCTT	780			
DB	3855	CGGGTTTATCATATCTCTCTTAACTCGCTGCTATAGCTCATCTTCTTATTTGGTCTT	3914			
QY	781	CTGCACTATCAAGATATGTGCGCTTGTCTCTTAATCCAGATCTTCAACACAGC	840			
DB	3915	CTGCACTATCAAGATATGTGCGCTTGTCTCTTAATCCAGATCTTCAACACACAGT	3974			
QY	841	ACGGGACCATGACGAGCTGACGACTCTGTCTCAAGAACTCTATGTTATCTTCTGT	900			

Db	3975	ACGGGACCATGCAAAACCTGCACACCTCGTCTCAAGGCAACTGTATGTTTCCCTCAGT	4034
QY	901	TGCTGTACAAACCTTGGATGGAACCTGACCTGTATTCACATCCCATATCTGGGCT	960
Db	4035	TGCTGTACAAACCTGACGATGGAATGTGACACCTGTATCCACATCCATCGTCTGGGCT	4094
QY	961	TTGGGAAAATTCATAGGGAGTGGGGCTCAGCCCGTTCTCCGGGCTCAGTTTACTAGT	1020
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1      RESULT 12
2      US-08-715-808-6
3      Sequence 6, Application US/08715808
4      Patent No. 5981274
5      GENERAL INFORMATION:
6      APPLICANT: Tyrrell, D. Iorine J.
7      APPLICANT: Chaisomchit, Sumonta
8      APPLICANT: Chang, Lung-ji
9      TITLE OF INVENTION: Recombinant Hepatitis Virus Vectors
10     NUMBER OF SEQUENCES: 16
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Medlen & Carroll, LLP
13     STREET: 220 Montgomery Street, Suite 2200
14     CITY: San Francisco
15     STATE: California
16     COUNTRY: United States of America
17     ZIP: 94104
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/715, 808
25     FILING DATE: 18-SEP-1996
26     CLASSIFICATION: 435
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Ingolia, Diane E.
29     REGISTRATION NUMBER: 40, 027
30     REFERENCE/DOCKET NUMBER: CHANG-02441
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: (415) 705-8410
33     TELEFAX: (415) 397-8338
34     INFORMATION FOR SEQ ID NO: 6:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 9859 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: double
39     TOPOLOGY: circular
40     MOLECULE TYPE: other nucleic acid
41     DESCRIPTION: /desc = "DNA"
42     US-08-715-808-6

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	Query Match	84.7%	Score 1000.2	DB 2	Length 9859
	Best Local Similarity	90.4%	Pred. No. 6.7e-294		
	Matches 1068	Conservative 0	Mismatches 113	Indels 0	Gaps 0
QY	1	ATGGGGAGAAATCTTTCCACCAGCAATCTTGGGATTTCTTTCCGACACCACTTGGAT	60		

Db 3402 ATGGGAGCAATCTTTCTGTTCCCAATCTTGGGATTTCTTCCCATCATCAAGTTGAC 3461
QY 61 CCAGCCTTCAGAGCAAAACCAACAATCCAGATTGGACCTTCAATCCCAACAGAGACAC 120
Db 3462 CCTGCATTTGGAGCAACTCAAAACATCCAGATTGGGACTTCAACCCCGTCAAGAGAC 3521
QY 121 TGGCAGACGCAACAAAGTTAGAGCTGGAGCATTCCGACTGGGGTTACCCACCGCAC 180
Db 3522 TGGCAGACGCAACAAAGTTAGAGCTGGAGCATTCCGAGCCCAAGCTCACCCCTCCAC 3581
QY 181 GGAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATTAACAACAACTTGGCAGCAAT 240
Db 3582 GGGGTTATTTGGGGTGGAGCCCTCAGGCTCAGGGCAATTTAGCAACAGTTCAACAATT 3641
QY 241 CCGCCTCTGCTTCCACCAATCGCCAGTCAGAGAGAGAGCCTACCCGCTGTCTCAACT 300
Db 3642 CCTCCTCTGCTTCCACCAATCGCCAGTCAGAGAGAGAGCCTACCTCCATCTCTCCACT 3701
QY 301 TTGAGAAACACTCATCTCTCAAGCATGAGTGAATCTCCACACTTTCCACCAACTCTG 360
Db 3702 CTAGAGACAGTCATCTCTCAGGCGCATGAGTGAATTTCACTGCTTCCACCAACTCTG 3761
QY 361 CAAGATCCAGAGAGAGCTGATTTCCCTGCTGCTGCTCAGTTCCAGAGACAGTA 420
Db 3762 CAGATCCAGAGAGAGCTGATTTCTGCTGCTGCTGCTCAGTTCCAGAGACAGTA 3821
QY 421 AACCTGTTCGCACTACTGCTCTCCATATGTCATTTCTCGAGGATTTGGGAGACCT 480
Db 3822 AACCTGTTCGCAATATTGCTCTCAGATCTGTCATCTCCGAGAGAGCTGGGAGACCT 3881
QY 481 GCGCGAAACATGGAACATCATCAGAGATTTCTAGAGACCTGCTGCTGTTACAGGCG 540
Db 3882 GTGACGAACATGGAACATCATCAGAGATTTCTAGAGACCTGCTGCTGTTACAGGCG 3941
QY 541 GGGTTTTCTTGTGAAGAAATCTCTCAATACCGAGAGCTAGAGCTGCTGCTGCTGCT 600
Db 3942 GGGTTTTCTTGTGAAGAAATCTCTCAATACCGAGAGCTAGAGCTGCTGCTGCTGCT 4001
QY 601 TCTCTCAATTTCTAGGGGGAATACCGTGTGCTTGGCCAAATTTGGCAGTCCCAACC 660
Db 4002 TCTCTCAATTTCTAGGGGGAATACCGTGTGCTTGGCCAAATTTGGCAGTCCCAACC 4061
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Db 4182 CTGCACTATCAAGGATATGTTGCCGTTTGTCTCTAAATTCAGAGATCAACAACAAGC 4241
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QY 1081 ATGTGTATCTGGGGGCAAGCTCTTACACATCTTGAAGTCCCTTTTACCGGCTGTACCA 1140
Db 4482 ATGTGTATCTGGGGGCAAGCTCTTACACATCTTGAAGTCCCTTTTATACCGGCTGTACCA 4541

QY 1141 ATTTTCTTTTGTCTTTGGGATATCAATTTAAACCTTATATA 1181
Db 4542 ATTTTCTTTTGTCTCTGGGATATCAATTTAAACCTTATATA 4582
RESULT 13
5196194-15
Patent No. 5196194
APPLICANT: RUTHER, WILLIAM J.; GOODMAN, HOWARD M.
TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,621
FILING DATE: 7-DEC-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 513,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 107,267
FILING DATE: 21-DEC-1979
APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979
SEQ ID NO:15:
LENGTH: 3220
5196194-15
Query Match 83.7%; Score 988.2; DB 6; Length 3220;
Best Local Similarity 90.3%; Pred. No. 1,7e-290;
Matches 1067; Conservative 0; Mismatches 113; Indels 1; Gaps 1;
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QY 181 GAGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCAATTAACAACCTTGCAGCAAT 240
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QY 241 CCGCCTCTGCTTCCACCAATGCGCAGTCAAGAGAGAGAGCTTCCCGCTGCTCCACT 300
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QY 661 TCATCACTACCAACCTCCGTCTCTCCAACTTGTCTCGGTTATCGCTGATGTGTCTG 720
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QY 721 CGGCGTTTATCATCTTCCCTCTTCACTCCGTCTGATGACCTTCATCTTGTGTGTTCT 780
Db 1795 CGGCGTTTATCATCTTCCCTCTTCACTCCGTCTGATGACCTTCATCTTGTGTGTTCT 1855
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RESULT 14
US-08-715-808-13
Sequence 13, Application US/08715808
Patent No. 5981274
GENERAL INFORMATION:
APPLICANT: Tyrrell, D. Lorne J.
APPLICANT: Chaisomchit, Sumonta
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Recombinant Hepatitis Virus Vectors
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08715, 808
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO. 13:
SEQUENCE CHARACTERISTICS:

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DB	3735	CCTGTATTCCGAGGCCAATCAAAACATCCAGATTGGGACTTCAACCCCATCAAGGACACC	379	
QY	121	TGGCCAGACGCCCAACAGGTAGAGCTGGAGCATTCCGACTGGGGTTCAACCCACCCGAC	180	
DB	3795	TGGCCAGACGCCCAACAGGTAGAGCTGGAGCATTCCGAGCCAGGGTTCAACCCCTCCACAC	385	
QY	181	GGAGGACCTTTGGGGGTGGAGCCCTCAGGCTCAGGGCATTAACCAAAACCTTGCAGCAAT	240	
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DB	3975	CTAAGAGACATCTCTCAGGACATGAGTGAATTCACATGCTTCCACCAAGCTCTG	403	
QY	361	CAAAATCCCAAGTGAAGAGTCTGATTTCCCTGCTGGTGGCTCCAGTTCAAGAACAGTA	420	
DB	4035	CAAAATCCCAAGTGAAGAGTCTGATTTCCCTGCTGGTGGCTCCAGTTCAAGAACAGTA	409	
QY	421	AACCTGTTCGCACTAGTCTCTCCCATTCGTCAATCTTTCGAGGATTGGGGACCT	480	
DB	4095	AACCTGTTCGCAATATTGCTCTCTCAATCTCTGTAATCTTCGCAAGACCGGGACCTT	415	
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Db 4695 CCATTTGTCAGTGGTTCGTAGGGCTTTCCCACTGTTGGCTTTCAGTTTATATGAGATG 4754
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QY 1141 ATTTCTTTGTCCTTTGGGATATACATTTAAACCTTAATAA 1181
Db 4815 ATTTCTTTGTCCTTTGGGATATACATTTAAACCTTAATAA 4855
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RESULT 15

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US-08-890-735C-1
; Sequence 1, Application US/08890735C
; Patent No. 6518014
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HEPADNAVIRUS CORES
; FILE REFERENCE: DC44A
; CURRENT APPLICATION NUMBER: US/08/890,735C
; CURRENT FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3182
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
US-08-890-735C-1
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Query Match 68.7%; Score 811.2; DB 4; Length 3182;
Best Local Similarity 97.3%; Pred. No. 1.2e-236;
Matches 825; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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Db 1 AATTCCACAACCTTCCACCAAACTCTGCAGATCCCAAGTGAAGGTCTGTATTTCCCT 60
QY 394 GCTGGTGGCTCCATTTAGAGAAAGTAACCTGTCGACTACTGTCTCCCATATCG 453
Db 61 GCTGGTGGCTCCATTTAGAGAAAGTAACCTGTCGACTACTGTCTCCCATATCG 120
QY 454 TCAATCTTCTGAGGATTTGGGACCTGCGCGGAACATGAGAAATCATCATCAGATTG 513
Db 121 TCAATCTTCTGAGGATTTGGGACCTGCGCGGAACATGAGAAATCATCATCAGATTG 180
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QY 694 TGTCTCTGTTATCGCTGAGATGTGTGCGGCGTTTATCATCTTCTCTCATCTGCTG 753
Db 361 TGTCTCTGTTATCGCTGAGATGTGTGCGGCGTTTATCATCTTCTCTCATCTGCTG 420
QY 754 CTATGCGCATCTCTTGTGTTCTTCTGAGCTATCAAGGATATGCGCGTTTGTCT 813
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QY 934 TGTATTCATATCCCATCATCTGAGGCTTTGGAAAAATTCCTATGGAGTGGGCTCAGCC 993
Db 601 TGTATTCATATCCCATCATCTGAGGCTTTGGAAAAATTCCTATGGAGTGGGCTCAGCC 660
QY 994 CGTTTCTCTGCTCAGATTACTAGTGCATTTGTCAGTGTTCGTAGGGCTTTTCCCC 1053
Db 661 CGTTTCTCTGCTCAGATTACTAGTGCATTTGTCAGTGTTCGTAGGGCTTTTCCCC 720
QY 1054 ACTGTTGGCTTTCAGTTATATGATGATGTGTACTGGGGGCCAAGTCTGTACACATC 1113
Db 721 ACTGTTGGCTTTCAGTTATATGATGATGTGTACTGGGGGCCAAGTCTGTACACATC 780
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Db 841 CTAATAA 848
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Search completed: September 15, 2003, 02:59:48
Job time : 76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 02:24:56 ; Search time 258 Seconds

(without alignments)
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Title: US-09-821-877-1

Perfect score: 1181
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Gapop 10.0, Gapext 1.0

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Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1181	100.0	1181	10	US-09-821-877-1 Sequence 1, Appli
2	1128.2	95.5	8007	9	US-09-837-297-3 Sequence 3, Appli
3	1001.8	84.8	4084	11	US-09-781-891D-21 Sequence 21, Appli
4	1001.8	84.8	4496	11	US-09-781-891D-22 Sequence 22, Appli
5	962.2	81.5	1286	12	US-10-136-819-1 Sequence 1, Appli
6	962.2	81.5	1286	14	US-10-132-829-3 Sequence 3, Appli
7	813.2	68.9	8717	9	US-09-837-297-4 Sequence 4, Appli
8	811.2	68.7	3182	10	US-09-929-955-14 Sequence 14, Appli
9	811.2	68.7	3182	13	US-10-104-966-11 Sequence 14, Appli
10	810.8	68.7	846	10	US-09-247-890-11 Sequence 11, Appli
11	756.4	64.0	846	10	US-09-247-890-9 Sequence 9, Appli
12	755.4	64.0	3221	11	US-10-209-264-1 Sequence 13, App
13	744.6	63.0	3215	14	US-10-209-264-1 Sequence 1, Appli
14	693	58.7	5618	14	US-10-142-358-1 Sequence 6, Appli
15	690	58.4	690	10	US-09-821-877-6 Sequence 7, Appli
16	675.6	57.2	690	10	US-09-821-877-7

17	668.2	56.6	681	10	US-09-821-877-3	Sequence 3, Appli
18	659.8	55.9	5130	10	US-09-897-006-9	Sequence 9, Appli
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20	652.2	55.2	681	9	US-09-812-862-13	Sequence 13, Appli
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25	412	34.9	426	10	US-09-247-890-15	Sequence 15, Appli
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27	411.6	34.9	426	11	US-09-781-891D-14	Sequence 14, Appli
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33	394	33.4	426	11	US-09-781-891D-20	Sequence 20, Appli
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41	326.6	27.7	870	9	US-09-812-862-7	Sequence 7, Appli
42	320.2	27.1	7991	9	US-09-837-297-5	Sequence 5, Appli
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44	195	16.5	235	9	US-09-837-297-1	Sequence 1, Appli
45	171	14.5	182	10	US-09-821-877-4	Sequence 4, Appli

ALIGNMENTS

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; Sequence 1, Application US/09821877
; Patent No. US20020177124A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Coleman, Paul F.
; APPLICANT: Mushawar, Isa K.
; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
; FILE REFERENCE: 6794.US.O1
; CURRENT APPLICATION NUMBER: US/09/821.877
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1181
; TYPE: DNA
; ORGANISM: Hepatitis B Virus
US-09-821-877-1

Query Match      100.0%; Score 1181; DB 10; Length 1181;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGGCAGAAATCTTCCACGAGCAATCTTGGGATTTCTCCGACCAAGTTGGAT 60
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Db 361 CAAGATCCCAAGTGAAGGTCTGTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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RESULT 2

US-09-837-297-3

; Sequence 3, Application US/09837297

; Patent No. US20010049143A1

; GENERAL INFORMATION:

; APPLICANT: RYU, WANG SHICK

; TITLE OF INVENTION: Hepatitis B virus vectors for gene therapy
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/837,297
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: KR2000-21070
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Kopatentlin 1.71
; SEQ ID NO 3
; LENGTH: 8007
; TYPE: DNA
; ORGANISM: HBV
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)-(8007)
; OTHER INFORMATION: Prototype vector of HBV
US-09-837-297-3

Query Match 95.5%; Score 1128.2; DB 9; Length 8007;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1148; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY 121 TGCGCAGACGCAACAGGATGAGGCTGAGCATTCGAGCTGGGGTTCAACCCGCGAC 180
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Db 1391 CAAGATCCCAAGTGAAGGTCTGTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1450
QY 421 AACCTGTTCCGACTACTGTCTCTCCATATGCTCAATCTTCTGAGATTTGGGAGACCT 480
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RESULT 3
US-09-781-891D-21
; Sequence 21, Application US/09781891D
; Publication No. US20030096222A1

; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomewsz, Angelina
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; PRIORITY FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 4084
; TYPE: DNA
; ORGANISM: HBV 1.28 genome
; US-09-781-891D-21

Query Match 84.8%; Score 1001.8; DB 11; Length 4084;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 ATGGGAGAAATCTTTCACAGCAATCTCTGGGATCTTTCACGACCCAGTTGAT 60
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QY 61 CCAGCTTCAGAGCAAAACCAACAATCCAGATTGGGACTTCAATCCCAACAAGACAC 120
Db 1496 CCGATTCGAGGCACTCAACCAATCCAGATTGGGACTTCAACCCCAACAAGACAC 1555
QY 121 TGCCAGACGCAACAAGATGAGAGCTGAGCATTCGAGCTGGGGTTCAACCCACGAC 180
Db 1556 TGCCAGACGCAACAAGATGAGAGCTGAGCATTCGAGCTGGGGTTCAACCCACGAC 1615
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QY 301 TTGAGAAACACTCATCTCTCAAGCCATGAGTGAATCTCAACAATTTTCAACCAACTCTG 360
Db 1736 TTGAGAAACACTCATCTCTCAAGCCATGAGTGAATCTCAACAATTTTCAACCAACTCTG 1795
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QY 481 GCGCGAAATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTACAGGCG 540
Db 1916 GTAGGAACATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTACAGGCG 1975
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Db 1976 GGGTTTTCTTGTGACAAAGATCTCTCAATACCGAGAGTCTGACTCGTGAGACT 2035
QY 601 TCTCTCAATTTCTATGAGGGGAACTACCGTGTGTCTGAGCAAAATTCGACGCCAAC 660
Db 2036 TCTCTCAATTTCTATGAGGGGAACTACCGTGTGTCTGAGCAAAATTCGACGCCAAC 2095
QY 661 TCCAAATCACTACCAACCTCTGCTCAACCTTGTCTGTATGCTGTAGTGTCTG 720
Db 2096 TCCAAATCACTACCAACCTCTGCTCAACCTTGTCTGTATGCTGTAGTGTCTG 2155
QY 721 CCGGCTTTTATCATTTCTCTCTCATCTGCTGTATGCTGTATGCTGTATGCTGT 780
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QY 781 CTGACATCAAGGATGTTGCGGCTTGTCTCTCAATTCAGAGATCTTCAACACACAGC 840
Db 2216 CTGACATCAAGGATGTTGCGGCTTGTCTCTCAATTCAGAGATCTTCAACACACAGC 2275
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QY 1021 CCATTGTTCACTGTTGTGATGAGGCTTTCCCACTGTTGGCTTTCAGTTATGATG 1080
Db 2456 CCATTGTTCACTGTTGTGATGAGGCTTTCCCACTGTTGGCTTTCAGTTATGATG 2515
QY 1081 ATGTGATCTGGGGGCAAGTCTGTACAGCAATCTGAGATCGGATCTTATACCGCTGTACCA 1140
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RESULT 4
US-09-781-891D-22
; Sequence 22, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister


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; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomew, Angelina
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 4496
; TYPE: DNA
; ORGANISM: HBV 1.5 genome
US-09-781-891D-22

Query Match      84.8%; Score 1001.8; DB 11; Length 4496;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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QY      61 CCAGCCTTCAGAGCAACACCAACATCCAGATTGGGACTTCAATCCCAACAGAGACACC 120
      1908 CTGCAATTCGAGGCAACTCAACATCCAGATTGGGACTTCAACCCCATCAAGGACAC 1967
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      1968 TGGCCAGACGCCCAACAGATGAGAGCTGAGCATTCGGGCGAGGCTCACCCCTCCAC 2027
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QY      241 CCGGCTCTCTGCTTCACCAATCGCAGTCAAGGAGGAGGAGCCGCTGCTTCACCT 300
      2088 CCTCTCTCTGCTTCACCAATCGCAGTCAAGGAGGAGGAGCCGCTGCTTCACCT 2147
QY      301 TTGAGAAACATCTCTCTCAAGCATGAGTGAATCCCAACTTTCCCAAACTCTG 360
      2148 CTAGAGACAGTCACTCTCAGGCGCATCAGTGAATTCCTGCTTCACCAAGCTCTG 2207
QY      361 CAAGATCCAGAGTGAAGTCTGTATTTCCCTGCTGATGAGTCAAGTCAAGACAGTA 420
      2208 CAGATCCAGAGTGAAGTCTGTATTTCCCTGCTGATGAGTCAAGTCAAGACAGTA 2267
QY      421 AACCTGTTCGACTGCTCTCTCCATATCGTCAATCTTTCGAGGATTTGGGACCT 480
      2268 AACCTGTTCGACTGCTCTCTCCATATCGTCAATCTTTCGAGGATTTGGGACCT 2327
QY      481 GCGCGAAACATGAGAACATCACTCAGATTTCTTGAAGACCCCTGCTCTGTTTCAAGCG 540
      2328 GTAGCAACATGAGAACATCACTCAGATTTCTTGAAGACCCCTGCTCTGTTTCAAGCG 2387
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QY      601 TCTCTCAATTTTCTAGGGGGAACGATCGTGTCTTGGCCAAATTTGCAAGTCCCAAC 660
      2448 TCTCTCAATTTTCTAGGGGGAACGATCGTGTCTTGGCCAAATTTGCAAGTCCCAAC 2507
QY      661 TCCATTAATCACTCAACAACTCTGTCTTCAACTTGTCTGTATTCGTGATGTGTCTG 720
      2508 TCCATTAATCACTCAACAACTCTGTCTTCAACTTGTCTGTATTCGTGATGTGTCTG 2567
QY      721 CGGGCTTTTATCATCTTCTCTCATCGTGTGATAGCCATCTTCTTGTGGTCTT 780
      2568 CGGGCTTTTATCATCTTCTCTCATCGTGTGATAGCCATCTTCTTGTGGTCTT 2627

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QY      781 CTGAGCATCAAGTATGTTGCCCGTTTGTCTCTTAATTCAGAGATCTTCAACACAGC 840
      2628 CTGAGTATCAAGTATGTTGCCCGTTTGTCTCTTAATTCAGAGATCTTCAACACAGC 2687
QY      841 ACGGACCATGAGACCTGACAGACTCTGCTCAAGAACTCTATGATCCCTCTGT 900
      2688 ACGGACCATGAGACCTGACAGACTCTGCTCAAGAACTCTATGATCCCTCTGT 2747
QY      901 TGTCTACAAAACCTTCGAGTGAACCTGACCTGTATTTCCATCCCATCTGCTGGCT 960
      2748 TGTCTACAAAACCTTCGAGTGAACCTGACCTGTATTTCCATCCCATCTGCTGGCT 2807
QY      961 TTGGAAAATTTCTATAGGAGTGGGCTCAGCCCTTCTCTGCTGCTCAAGTAA 1020
      2808 TTGGAAAATTTCTATAGGAGTGGGCTCAGCCCTTCTCTGCTGCTCAAGTAA 2867
QY      1021 CCATTTGTCAGTGTTCGAGGCTTTCCCCCACTTTGGCTTCAATATATAGATG 1080
      2868 CCATTTGTCAGTGTTCGAGGCTTTCCCCCACTTTGGCTTCAATATATAGATG 2927
QY      1081 ATGTTGTAATGAGGAGGCAATCTGTACACATCTTGAATCCCTTTTACCGCTGTACCA 1140
      2928 ATGTTGTAATGAGGAGGCAATCTGTACACATCTTGAATCCCTTTTACCGCTGTACCA 2987
QY      1141 ATTTTCTTTTGTCTTTGGTATTCATTTAAACCTTAATAA 1181
      2988 ATTTTCTTTTGTCTTTGGTATTCATTTAAACCTTAATAA 3028

RESULT 5
US-10-136-819-1
; Sequence 1, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific ger
; FILE REFERENCE: 6627-PAL198
; CURRENT APPLICATION NUMBER: US/10/136,819
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-136-819-1

Query Match      81.5%; Score 962.2; DB 12; Length 1286;
Best Local Similarity 89.3%; Pred. No. 1,7e-302;
Matches 1055; Conservative 0; Mismatches 108; Indels 18; Gaps 1;

QY      1 ATGGGCGAGATCTTTTCACAGCAATCTCTTGGGATTTCTTCCGACACAGTTGGAT 60
      119 ATGGGCGAGATCTTTCTGTCTTCCAAATCTCTGGGATTTCTTCCATCAACAGTTGGAC 178
QY      61 CCAGCCTTCAGAGCAACACCAACATCCAGATTGGGACTTCAATCCCAACAGAGACACC 120
      179 CCGCGTTTGGAGCCCACTAAACATTCAGATTGGGACTTCAACCCCAACAGAGATCAA 238
QY      121 TGGCCAGACGCCCAACAGTGAAGCTGAGCATTCGAGCTGGGGTTCACCCGACCGCAC 180
      239 TGGCCAGAGCAATATCAGTGAAGAGGGGAGCATTTGGGGCAGAGGTTCAACCCACACAC 298
QY      181 GAGAGCCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAAACCTTGGCCAGCAAT 240
      299 GGGGCTTTTGGGGTGGAGCCCTCAGGCTCAGGGCATTAACAAACAGTCCAGCAGCA 358
QY      241 CCGCTCTCTGCTTCACCAATGCGCAGTCAAGGAGGAGGAGCCGCTGCTGTCCACCT 300
      359 CCGCTCTCTGCTTCACCAATGCGCAGTCAAGGAGGAGGAGCCGCTGCTGTCCACCT 418

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301 TTGAGAACTCATCTCAAGCCATGAGTGAATCTCCAACTTTCCACCAACTCTG 360
419 CTAAAGACAGTCACTCTAGGSCATGAGTGAATCCAAACATTCACCAACTCTG 478
361 CAAGATCCCAAGTGAAGTGTGATTTCCCTGCTGAGTCCAGTTCAAGAAACAGTA 420
479 CTAGATCCCAAGTGAAGTGTGATTTCCCTGCTGAGTCCAGTTCAAGAAACAGTA 538
421 AACCTGTTCGACATCTCTCTCCATATGTCATCTTCCAGATTTGGGACCT 480
539 AACCTGTTCGACATCTCTCTCCATATGTCATCTTCCAGATTTGGGACCT 580
481 GCGCGAATCATGAGAAACATCAATCAGATTCTAGAACCCCTGCTGTTACAGGCG 540
581 GCACCGAATCATGAGAAACATCAATCAGATTCTAGAACCCCTGCTGTTACAGGCG 640
541 GGGTTTTTCTGTGACAAAGATCTTCAATACCGCAGAGTCTAGACTGTGTGACT 600
641 GGGTTTTTCTGTGACAAAGATCTTCAATACCGCAGAGTCTAGACTGTGTGACT 700
601 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 660
701 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 760
661 TCCATCACTACCAACCTCTGCTCCCACTTGTGCTGTTATCGCTGATGTGTCTG 720
761 TCCATCACTACCAACCTCTGCTCCCACTTGTGCTGTTATCGCTGATGTGTCTG 820
721 CGGCGTTTTATCATCTTCTTCAATCTGCTGATGCTGATGCTGCTTCTTGTGTTCT 780
821 CGGCGTTTTATCATCTTCTTCAATCTGCTGATGCTGATGCTGCTTCTTGTGTTCT 880
781 CTGAGCTATCAAGATGATGTGCGCGTTTGTCTTATTCAGATCTTCAACACACACG 840
881 CTGAGCTATCAAGATGATGTGCGCGTTTGTCTTATTCAGATCTTCAACACACACG 940
841 ACGGACCATGAGAGGCTCTGCTGCTCAAGAACTCTATGATCCCTCCCTG 900
941 ACGGACCATGAGAGGCTCTGCTGCTCAAGAACTCTATGATCCCTCCCTG 1000
901 TCTCTCAAAACCTTCCGATGAGAACTGACCTGATTTCCATCCATCATCTCTGAGCT 960
1001 TCTCTCAAAACCTTCCGATGAGAACTGACCTGATTTCCATCCATCATCTCTGAGCT 1060
961 TTGCGAAATTTCTATGAGAGTGTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1061 TTGCGAAATTTCTATGAGAGTGTGAGCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTG 1120
1021 CCATTTGTCAGTGTGTCGAGGCTTTCCCACTGTTGCTTCACTTATGAGAGT 1080
1121 CCATTTGTCAGTGTGTCGAGGCTTTCCCACTGTTGCTTCACTTATGAGAGT 1180
1081 ATGTTGTCAGTGTGTCGAGGCTTCTGACATCTTGAAGTCCCTTTTACCGCTGTTACCA 1140
1181 ATGTTGTCAGTGTGTCGAGGCTTCTGACATCTTGAAGTCCCTTTTACCGCTGTTACCA 1240
1141 ATTTTCTTTTGTCTTGGTATATTAATTAACCTTATTA 1181
1241 ATTTTCTTTTGTCTTGGTATATTAATTAATTAATTA 1281

RESULT 6
US-10-132-829-3
; Sequence 3, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to create hemophilia by hepatic gene transfer of Factor VII
; FILE REFERENCE: 6627-Pa1170
; CURRENT APPLICATION NUMBER: US/10/132,829

; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 3
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-132-829-3
Query Match 81.5%; Score 962.2; DB 14; Length 1286;
Best Local Similarity 89.3%; Pred. No. 1.7e-302;
Matches 1055; Conservative 0; Mismatches 108; Indels 18; Gaps 1;
1 ATGGGAGCAATCTTCCACGCAATCTCTGGATCTTCCGACCACTGAT 60
119 ATGGGAGCAATCTTCCACGCAATCTCTGGATCTTCCGACCACTGAT 178
61 CCAGCTTCAGAGCAACCAACCAATCAGATTGGACTTCAATCCCAAGAGAC 120
179 CTGCGTTTCGAGCCCACTCAACCAATCAGATTGGACTTCAATCCCAAGAGAC 238
121 TGCGCAGAGCCCAACCAATCAGATTGGACTTGGACTTCAATCCCAAGAGAC 180
229 TGCGCAGAGCCCAACCAATCAGATTGGACTTGGACTTCAATCCCAAGAGAC 298
181 GAGGCTTTTGGGTTGAGGCTTCAAGCTCAGGCTATCAACCAATCTGACCAAT 240
239 GAGGCTTTTGGGTTGAGGCTTCAAGCTCAGGCTATCAACCAATCTGACCAAT 358
241 CGGCTCTGCTTCCCAATTCGAGCAAGAGGAGGCTTCCGCTGCTCAGCT 300
359 CTCTCTCTGCTTCCCAATTCGAGCAAGAGGAGGCTTCCGCTGCTCAGCT 418
301 TTGAGAACTCATCTCAAGCCATGAGTGAATCTCCAACTTTCCACCAACTCTG 360
419 CTAAAGACAGTCACTCTAGGSCATGAGTGAATCCAAACATTCACCAACTCTG 478
361 CAAGATCCCAAGTGAAGTGTGATTTCCCTGCTGAGTCCAGTTCAAGAAACAGTA 420
479 CTAGATCCCAAGTGAAGTGTGATTTCCCTGCTGAGTCCAGTTCAAGAAACAGTA 538
421 AACCTGTTCGACATCTCTCTCCATATGTCATCTTCCAGATTTGGGACCT 480
539 AACCTGTTCGACATCTCTCTCCATATGTCATCTTCCAGATTTGGGACCT 580
481 GCGCGAATCATGAGAAACATCAATCAGATTCTAGAACCCCTGCTGTTACAGGCG 540
581 GCACCGAATCATGAGAAACATCAATCAGATTCTAGAACCCCTGCTGTTACAGGCG 640
541 GGGTTTTTCTGTGACAAAGATCTTCAATACCGCAGAGTCTAGACTGTGTGACT 600
641 GGGTTTTTCTGTGACAAAGATCTTCAATACCGCAGAGTCTAGACTGTGTGACT 700
601 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 660
701 TCTCTCAATTTCTAGGGGGAATCTACCGTGTCTTGGCCAAATTCGAGTCCCAACC 760
661 TCCATCACTACCAACCTCTGCTCCCACTTGTGCTGTTATCGCTGATGTGTCTG 720
761 TCCATCACTACCAACCTCTGCTCCCACTTGTGCTGTTATCGCTGATGTGTCTG 820
721 CGGCGTTTTATCATCTTCTTCAATCTGCTGATGCTGATGCTGCTTCTTGTGTTCT 780
821 CGGCGTTTTATCATCTTCTTCAATCTGCTGATGCTGATGCTGCTTCTTGTGTTCT 880
781 CTGAGCTATCAAGATGATGTGCGCGTTTGTCTTATTCAGATCTTCAACACACACG 840
881 CTGAGCTATCAAGATGATGTGCGCGTTTGTCTTATTCAGATCTTCAACACACACG 940
841 ACGGACCATGAGAGGCTCTGCTGCTCAAGAACTCTATGATCCCTCCCTG 900

Db 941 ACGGGCCATGCAAGACCTGACGATTCCTGCTCAAGAACTCTATGTTCCCTCTTGT 1000
QY 901 TGGCTATCAAAACCTTGATGAGAACTGCACTGTATTCATCCCATGATCCTGGGCT 960
Db 1001 TGGCTATCAAAACCTTGATGAGAACTGCACTGTATTCATCCCATGATCCTGGGCT 1060
QY 961 TTGGGAAATTCCTATGAGAGTGGGCTCAGCCGTTTCTGCTGCTCAGTTTACTATG 1020
Db 1061 TTGGCAGAGATTCCTATGAGAGTGGGCTCAGCTCGTTTCTGCTGCTCAGTTTACTATG 1120
QY 1021 CCATTTGTGATGAGTGTGATGAGGCTTCCGCCCATGTTGGGCTTTCAGTTATATGATG 1080
Db 1121 CCATTTGTGATGAGTGTGATGAGGCTTCCGCCCATGTTGGGCTTTCAGTTATATGATG 1180
QY 1081 ATGTTGATGAGGAGGCAAGTCTGTACACATCTTGAGTCCCTTTTACCGCTGTACCA 1140
Db 1181 ATGAGTATGAGGAGGCAAGTCTGTACACATCTTGAGTCCCTTTTACCGCTGTATTA 1240
QY 1141 ATTTTCTTTTGTCTTTGGGATATACATTTAAACCTTAATAA 1181
Db 1241 ATTTTCTTTTGTCTTTGGGATATACATTTAAATGAATTGAA 1281

RESULT 7

US-09-837-297-4
; Sequence 4, Application US/09837297
; Patent No. US20010049145A1
; GENERAL INFORMATION:
; APPLICANT: RYU, WANG SHICK
; TITLE OF INVENTION: Hepatitis B virus vectors for gene therapy
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/837,297
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: KR2000-21070
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 4
; LENGTH: 8717
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R711: pCMV-HBV/GFP Full Sequence
US-09-837-297-4

Query Match 68.9%; Score 813.2; DB 9; Length 8717;
Best Local Similarity 97.3%; Pred. No. 1,7e-253;
Matches 827; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 332 GGAATCCACAACTTTCCACCAAACTTGCAAGATCCAGAGTGAAGGTCTGTATTTC 391
Db 2072 GGAATTCACAACTTTCCACCAAACTTGCAAGATCCAGAGTGAAGGTCTGTATTTC 2131
QY 392 CTGCTGGTGGCTCAGTTCAGAAACAGTAACCTGTTCCGATCTACGTCTCCCATAT 451
Db 2132 CTGCTGGTGGCTCAGTTCAGAAACAGTAACCTGTTCCGATCTACGTCTCCCATAT 2191
QY 452 CGTCAATCTTCTGAGAGATTGGGAGCCCTGCGGGAACATGAGAAACATCAATCAGAT 511
Db 2192 CGTCAATCTTCTGAGAGATTGGGAGCCCTGCGGGAACATGAGAAACATCAATCAGAT 2251
QY 512 TCCTAGAGACCCCTGCTGCTGTACAGGCGGGGTTTCTTGTGACAAAGATCCTCAAA 571
Db 2252 TCCTAGAGACCCCTTCTGCTGTACAGGCGGGGTTTCTTGTGACAAAGATCCTCAAA 2311
QY 572 TACGAGAGAGTCTGATGAGTGTGAGTCTCTCAATTTTCTAGGGGGAACATACGTGT 631
Db 2312 TACGAGAGAGTCTGATGAGTGTGAGTGTCTCTCAATTTTCTAGGGGGAACATACGTGT 2371
QY 632 GTCTTGCCCAAAATTCGAGATCCCAACCTCAATCACTCAACAACTCTGTCTCCAA 691
Db 2372 GTCTTGCCCAAAATTCGAGATCCCAACCTCAATCACTCAACAACTCTGTCTCCAA 2431

QY 692 CTGTGCTGGTATGCTGTGAGTGTCTGGGCGTTTATCATCTTCTCTTCATCCTGC 751
Db 2432 CTGTGCTGGTATGCTGTGAGTGTCTGGGCGTTTATCATCTTCTCTTCATCCTGC 2491
QY 752 TGGTATGCCATCTTCTGTGTTGTTCTTCTGACATATCAAGTATGTTCCCGCTTGTG 811
Db 2492 TGGTATGCCATCTTCTGTGTTGTTCTTCTGACATATCAAGTATGTTCCCGCTTGTG 2551
QY 812 CTCTAATCCAGAGTCTTCAACACGAGACGGAACATGACAGAGCTGCACATCTG 871
Db 2552 CTCTAATCCAGAGTCTTCAACACGAGACGGAACATGACAGAGCTGCATGATCTG 2611
QY 872 CTCAAGAACTCTATGATATCCCTCTGTGCTGTACAAACCTTGATGAACTGCA 931
Db 2612 CTCAAGAACTCTATGATATCCCTCTGTGCTGTACAAACCTTGATGAACTGCA 2671
QY 932 CCGTATTCATCCATCCATCATCTCTGGGCTTGGGAAATTCCTATGAGAGTGGGCTCG 991
Db 2672 CCGTATTCATCCATCCATCATCTCTGGGCTTGGGAAATTCCTATGAGAGTGGGCTCG 2731
QY 992 CCGGTTTCTCGGCTCAGTTTACTAGTGCATTTGTCAGTGTGATAGGCTTTCC 1051
Db 2732 CCGGTTTCTCGGCTCAGTTTACTAGTGCATTTGTCAGTGTGATAGGCTTTCC 2791
QY 1052 CCACTGTTGGCTTTCAGTTATATGATATGATATGTTGATCGGGGCCAAGTCTGTACCA 1111
Db 2792 CCACTGTTGGCTTTCAGTTATATGATATGATATGATATGATGAGGCGCAAGTCTGTACCA 2851
QY 1112 TCTTGAAGTCCCTTTTACCGGCTTACCAATTTCTTGTGCTTGGGATACATTAA 1171
Db 2852 TCTTGAAGTCCCTTTTACCGGCTTACCAATTTCTTGTGCTTGGGATACATTAA 2911
QY 1172 CCCTAATAA 1181
Db 2912 CCCTAATAA 2921

RESULT 8

US-09-929-955-14
; Sequence 14, Application US/09929955
; Patent No. US20020136740A1
; GENERAL INFORMATION:
; APPLICANT: Catharina Hulstgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE REFERENCE: TRIPEP 23AUS2
; CURRENT APPLICATION NUMBER: US/09/929,955
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3182
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus sequence
US-09-929-955-14

Query Match 68.7%; Score 811.2; DB 10; Length 3182;

Best Local Similarity 97.3%; Pred. No. 4.3e-253;
Matches 825; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 334 AACTCACAAGCTTTCACCAAACTGCAAGATCCAGAGTGAAGGTGTATTTCCCT 393
Db 1 AATTCACAACCTTTCACCAAACTGCAAGATCCAGAGTGAAGGTGTATTTCCCT 60

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Qy 394 GCTGTGCTCCAGTTCAGAAACAGTAAACCTGTGTCGACTACTGTCTCCCATATG 453
Db 61 GCTGTGCTCCAGTTCAGAAACAGTAAACCTGTGTCGACTACTGTCTCCCATATG 120
Qy 454 TCAATCTTCTGAGATTTGGGGAACCTGCGGGAACATGGAACATCATCAGATTG 513
Db 121 TCAATCTTCTGAGATTTGGGGAACCTGCGGGAACATGGAACATCATCAGATTG 180
Qy 514 CTAGAACCCCTGCTGCTGTATACAGGCGGGGTTTTCTTTGTGACAAAGATCTCAATA 573
Db 181 CTAGAACCCCTGCTGCTGTATACAGGCGGGGTTTTCTTTGTGACAAAGATCTCAATA 240
Qy 574 CCGCAGAGCTAGACTCGTGTGAGACTTCTCAATTTTCTAGGGGGAACATCCGTGTG 633
Db 241 CCGCAGAGCTAGACTCGTGTGAGACTTCTCAATTTTCTAGGGGGAACATCCGTGTG 300
Qy 634 CTGGCCCAAAATTCGCAATGCCCAACCTCAATCACTACCAACCTCTCTCTCACT 693
Db 301 CTGGCCCAAAATTCGCAATGCCCAACCTCAATCACTACCAACCTCTCTCTCACT 360
Qy 694 TGTCTGCTATCGCTGATGTGTGCGGGGTTTTATATCTCTCTCAATCCGTGTG 753
Db 361 TGTCTGCTATCGCTGATGTGTGCGGGGTTTTATATCTCTCTCAATCCGTGTG 420
Qy 754 CTATGCTCATCTCTGTGTGCTTCTGACATCAAGATATGTCCTGTGTCT 813
Db 421 CTATGCTCATCTCTGTGTGCTTCTGACATCAAGATATGTCCTGTGTCT 480
Qy 814 CTAAATCCAGATCTTCAACCAACAGCAGCAGGACCAATGACAGCTCTGCT 873
Db 481 CTAAATCCAGATCTTCAACCAACAGCAGCAGGACCAATGACAGCTCTGCT 540
Qy 874 CAAGAACCTCATGATATCCCTGCTGTGACAAACCTCGAATGGAACCTGACAC 933
Db 541 CAAGAACCTCATGATATCCCTGCTGTGACAAACCTCGAATGGAACCTGACAC 600
Qy 934 TGTATTTCCATCCCATCATCTGAGGCTTGGAAAAATTCATAGGAGTGGCTCAGCC 993
Db 601 TGTATTTCCATCCCATCATCTGAGGCTTGGAAAAATTCATAGGAGTGGCTCAGCC 660
Qy 994 CGTTTCTCTGCTCAATTTACTAGTGCATTTGTCAATGTTGTGAGGGCTTTTCCCC 1053
Db 661 CGTTTCTCTGCTCAATTTACTAGTGCATTTGTCAATGTTGTGAGGGCTTTTCCCC 720
Qy 1054 ACTGTTGCTTCAATATATGATGATGTGCTGAGGGGCAAGCTGTACACCATC 1113
Db 721 ACTGTTGCTTCAATATATGATGATGTGCTGAGGGGCAAGCTGTACACCATC 780
Qy 1114 TTGAGTCCCTTTTACCGCTGTACCAATTTTCTTTGTGTTGGGTATACATTTAAAC 1173
Db 781 TTGAGTCCCTTTTACCGCTGTACCAATTTTCTTTGTGTTGGGTATACATTTAAAC 840
Qy 1174 CTAAATPAA 1181
Db 841 CTAAACAA 848

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RESULT 9
US-10-104-966-14
; Sequence 14, Application US/10104966
; Publication No. US20020155124A1
; GENERAL INFORMATION:
; APPLICANT: Matsi Salberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE REFERENCE: TRIPEP. 23AUSCI
; CURRENT APPLICATION NUMBER: US/10/104, 966
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/705, 547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229, 175
; PRIOR FILING DATE: 2000-08-29

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3182
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus sequence
US-10-104-966-14

Query Match      68.7%; Score 811.2; DB 13; Length 3182;
Best Local Similarity 97.3%; Pred. No. 4.3e-253;
Matches 825; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 334 AACTCCACAACCTTCCACCAACCTCGAAGATCCCAAGTGAAGGTGTGATTTCCCT 393
Db 1 AATTCACAACTTCCACCAACCTTGAAGATCCCAAGTGAAGGTGTGATTTCCCT 60
Qy 394 GCTGTGCTCCAGTTCAGAAACAGTAAACCTGTGTCGACTACTGTCTCCCATATG 453
Db 61 GCTGTGCTCCAGTTCAGAAACAGTAAACCTGTGTCGACTACTGTCTCCCATATG 120
Qy 454 TCAATCTTCTGAGATTTGGGGAACCTGCGGGAACATGGAACATCATCAGATTG 513
Db 121 TCAATCTTCTGAGATTTGGGGAACCTGCGGGAACATGGAACATCATCAGATTG 180
Qy 514 CTAGAACCCCTGCTGCTGTATACAGGCGGGGTTTTCTTTGTGACAAAGATCTCAATA 573
Db 181 CTAGAACCCCTGCTGCTGTATACAGGCGGGGTTTTCTTTGTGACAAAGATCTCAATA 240
Qy 574 CCGCAGAGCTAGACTCGTGTGAGACTTCTCAATTTTCTAGGGGGAACATCCGTGTG 633
Db 241 CCGCAGAGCTAGACTCGTGTGAGACTTCTCAATTTTCTAGGGGGAACATCCGTGTG 300
Qy 634 CTGGCCCAAAATTCGCAATGCCCAACCTCAATCACTACCAACCTCTCTCTCACT 693
Db 301 CTGGCCCAAAATTCGCAATGCCCAACCTCAATCACTACCAACCTCTCTCTCACT 360
Qy 694 TGTCTGCTATCGCTGATGTGTGCGGGGTTTTATATCTCTCTCAATCCGTGTG 753
Db 361 TGTCTGCTATCGCTGATGTGTGCGGGGTTTTATATCTCTCTCAATCCGTGTG 420
Qy 754 CTATGCTCATCTCTGTGTGCTTCTGACATCAAGATATGTCCTGTGTCT 813
Db 421 CTATGCTCATCTCTGTGTGCTTCTGACATCAAGATATGTCCTGTGTCT 480
Qy 814 CTAAATCCAGATCTTCAACCAACAGCAGCAGGACCAATGACAGCTCTGCT 873
Db 481 CTAAATCCAGATCTTCAACCAACAGCAGCAGGACCAATGACAGCTCTGCT 540
Qy 874 CAAGAACCTCATGATATCCCTGCTGTGACAAACCTCGAATGGAACCTGACAC 933
Db 541 CAAGAACCTCATGATATCCCTGCTGTGACAAACCTCGAATGGAACCTGACAC 600
Qy 934 TGTATTTCCATCCCATCATCTGAGGCTTGGAAAAATTCATAGGAGTGGCTCAGCC 993
Db 601 TGTATTTCCATCCCATCATCTGAGGCTTGGAAAAATTCATAGGAGTGGCTCAGCC 660
Qy 994 CGTTTCTCTGCTCAATTTACTAGTGCATTTGTCAATGTTGTGAGGGCTTTTCCCC 1053
Db 661 CGTTTCTCTGCTCAATTTACTAGTGCATTTGTCAATGTTGTGAGGGCTTTTCCCC 720
Qy 1054 ACTGTTGCTTCAATATATGATGATGTGCTGAGGGGCAAGCTGTACACCATC 1113
Db 721 ACTGTTGCTTCAATATATGATGATGTGCTGAGGGGCAAGCTGTACACCATC 780
Qy 1114 TTGAGTCCCTTTTACCGCTGTACCAATTTTCTTTGTGTTGGGTATACATTTAAAC 1173
Db 781 TTGAGTCCCTTTTACCGCTGTACCAATTTTCTTTGTGTTGGGTATACATTTAAAC 840
Qy 1174 CTAAATPAA 1181
Db 841 CTAAACAA 848

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RESULT 10
US-09-247-890-11
; Sequence 11, Application US/09247890
; Publication No. US20020198162A1
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juhua
; APPLICANT: Baes, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/09/247,890
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 60/074,294
; EARLIER FILING DATE: 1998-02-11
; EARLIER APPLICATION NUMBER: US 60/105,509
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(846)
; OTHER INFORMATION: Pres2-S coding region of hepatitis B virus alyw
; OTHER INFORMATION: Surface antigen (HBsAg)
US-09-247-890-11

Query Match      68.7%; Score 810.8; DB 10; Length 846;
Best Local Similarity 97.4%; Pred. No. 2.9e-253;
Matches 824; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY      325 ATGCAGTGAAGTCCACAACTTTCACAACTCTGCAGATCCAGAGTGAAGGTCTG 384
DB      1 ATGCAGTGAAGTCCACAACTTTCACAACTCTGCAGATCCAGAGTGAAGGTCTG 60
QY      385 TATTTCCCTGCTGCTGCTCCAGTTCAAGAACTAAACCTGTTCCGACTACTGCTCT 444
DB      61 TATTTCCCTGCTGCTGCTCCAGTTCAAGAACTAAACCTGTTCCGACTACTGCTCT 120
QY      445 CCCATATCGTCAATCTTCTGAGAGATGGGAGCCCTGCGGGGAAACATGGAACATCACA 504
DB      121 CCTTATCGTCAATCTTCTGAGAGATGGGAGCCCTGCGGGGAAACATGGAACATCACA 180
QY      505 TCAGATTCCTAGAGACCCCTGCTCGTGTTCACAGCGGGGTTTTCTTGTGACAAAGATC 564
DB      181 TCAGATTCCTAGAGACCCCTGCTCGTGTTCACAGCGGGGTTTTCTTGTGACAAAGATC 240
QY      565 CTACAAATACCGAGAGTCTAGACTCGTGTGCACTTCTCAATTTTCTAGGGGGAAT 624
DB      241 CTACAAATACCGAGAGTCTAGACTCGTGTGCACTTCTCAATTTTCTAGGGGGAAT 300
QY      625 ACCGTGCTGTGGCCAAATTCGAGTCCCAACCTCCAACTCACTACCAACCTCTCT 684
DB      301 ACCGTGCTGTGGCCAAATTCGAGTCCCAACCTCCAACTCACTACCAACCTCTCT 360
QY      685 CCTTCAACTTGTCTGCTGTTATCGTGTATGTCGCGGCTTTTATCATCTTCTCTTC 744
DB      361 CCTTCAACTTGTCTGCTGTTATCGTGTATGTCGCGGCTTTTATCATCTTCTCTTC 420
QY      745 ATCTGCTGTATGCTCATCTTCTGTTGTTCTTCTGACATACAGGTATGTTGCC 804
DB      421 ATCTGCTGTATGCTCATCTTCTGTTGTTCTTCTGACATACAGGTATGTTGCC 480
QY      805 GTTGTGCTCTAATTCAGAGATCTTCAACGACGAGGAGACCATGACAGGCTGACG 864
DB      481 GTTGTGCTCTAATTCAGAGATCTTCAACGACGAGGAGACCATGACGAGGCTGACG 540
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QY      865 ACTCTGCTCAAGAACCTTATGATCCCTCCTGTTGCTGACAAACCTTGGATGGA 924
DB      541 ACTAGCTCAAGAACCTTATGATCCCTCCTGTTGCTGACAAACCTTGGAGGGA 600
QY      925 AACTGCACTGTATTTCCATCCCATCATCTCTGGGCTTTGGAAATTTCTATGGAGTGG 984
DB      601 AATTGCACTGTATTTCCATCCCATCATCTCTGGGCTTTGGAAATTTCTATGGAGTGG 660
QY      985 GCTCAGCCGCTTCTCCTGAGCTCAGTTACTAGTSCCATTTGTTAGTGGTTCTGTAAGG 1044
DB      661 GCTCAGCCGCTTCTCCTGAGCTCAGTTACTAGTSCCATTTGTTAGTGGTTCTGTAAGG 720
QY      1045 CTTTCCCACTGTTGGCTTTCAGTTATATGATGATGTTACTGGGGCCCAAGTCTG 1104
DB      721 CTTTCCCACTGTTGGCTTTCAGTTATATGATGATGTTACTGGGGCCCAAGTCTG 780
QY      1105 TACACATCTTGAGTCCCTTTTAAACCGCTGTTACCAATTTTCTTTGTCTTTGGATAC 1164
DB      781 TACAGCATCTTGAGTCCCTTTTAAACCGCTGTTACCAATTTTCTTTGTCTTTGGATAC 840
QY      1165 ATTAA 1170
DB      841 ATTAA 846

RESULT 11
US-09-247-890-9
; Sequence 9, Application US/09247890
; Publication No. US20020198162A1
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juhua
; APPLICANT: Baes, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/09/247,890
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 60/074,294
; EARLIER FILING DATE: 1998-02-11
; EARLIER APPLICATION NUMBER: US 60/105,509
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(846)
; OTHER INFORMATION: Pres2-S coding region of hepatitis B virus adr
; OTHER INFORMATION: Surface antigen (HBsAg)
US-09-247-890-9

Query Match      64.0%; Score 756.4; DB 10; Length 846;
Best Local Similarity 93.4%; Pred. No. 1.5e-235;
Matches 790; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      325 ATGCATGGAAGTCCCAACTTTCACAACTCTGCAAGATCCAGAGTGAAGGTCTG 384
DB      1 ATGCATGGAAGTCCCAACTTTCACAACTCTGCAAGATCCAGAGTGAAGGTCTG 60
QY      385 TATTTCCCTGCTGCTGCTCCAGTTCAAGAACTAAACCTGTTCCGACTACTGCTCT 444
DB      61 TATTTCCCTGCTGCTGCTCCAGTTCAAGAACTAAACCTGTTCCGACTACTGCTCT 120
QY      445 CCCATATCGTCAATCTTCTGAGAGATGGGAGACCTGCGCGGAACTGAGAAACATCACA 504
DB      121 CCCATATCGTCAATCTTCTGAGAGATGGGAGACCTGCGCGGAACTGAGAAACATCACA 180
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QY 505 TCAGGATTCCTAGAGACCCCTGCTGTTACAGCGGGGTTTTCTGTTGACAAGATC 564
DB 181 TCAGGATTCCTAGAGACCCCTGCTGTTACAGCGGGGTTTTCTGTTGACAAGATC 240
QY 565 CTCACATACCGCAGAGTCTAGACTGTGTGTGAGACTTCTCTCATATTTCTAGGGGAACT 624
DB 241 CTCACATACCGCAGAGTCTAGACTGTGTGTGAGACTTCTCTCATATTTCTAGGGGAGCA 300
QY 625 ACCGCTGCTTGGCGAAATTCGCAAGTCCCAACTCCATCATCTACACCAACTCTCTGT 684
DB 301 CCGAGCTGTGGCGAAATTCGCAAGTCCCAACTCCATCATCTACACCAACTCTCTGT 360
QY 685 CCGCAACTCTGCTGTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 744
DB 361 CCGCAACTCTGCTGTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 420
QY 745 ATCTGCTGCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
DB 421 ATCTGCTGCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 805 GTTGTGCTCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
DB 481 GTTGTGCTCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 865 ACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924
DB 541 ACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 925 AACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984
DB 601 AACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 985 GCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
DB 661 GCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 1045 CTTTCCCCCAGCTGTTGGCTTCACTATGATGATGATGATGATGATGATGATGATGATG 1104
DB 721 CTTTCCCCCAGCTGTTGGCTTCACTATGATGATGATGATGATGATGATGATGATGATG 780
QY 1105 TACACCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164
DB 781 TACACCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 1165 ATTAA 1170
DB 841 ATTGA 846
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RESULT 12
US-09-848-616-133

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; Sequence 133, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Seibel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 133
; LENGTH: 3221
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1901)..(2458)
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US-09-848-616-133

Query Match 64.0%; Score 755.4; DB 11; Length 3221;
Best Local Similarity 93.4%; Pred. No. 6.6e-235;
Matches 789; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 337 TCACAACTTTTCACAAACTCTGCAGATCCAGAGTGAAGTCTGATTTCCCTGCT 396
DB 2 TCACAACTTTTCACAAAGCTCTGCAGACCCAGAGTGAAGTCTGATTTCCCTGCT 61
QY 397 GGTGCTCAGTTGACGAAACAGTAAACCTGTTCCGACTGCTGCTGCTGCTGCTGCTGCTG 456
DB 62 GGTGCTCAGTTGACGAAACAGTAAACCTGTTCCGAAATATGCTTACATCTGCTCA 121
QY 457 ATCTTCTGAGAGATGAGGAGCCCTGCGGGAACATGGAACATCATCATGAGATTCCTA 516
DB 122 ATCTCAGGAGACTGAGGAGCCCTGCTGACAAATGAGAAACATCATCATGAGATTCCTA 181
QY 517 GGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576
DB 182 GGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
QY 577 CAGAGTCTAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
DB 242 CAGAGTCTAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
QY 637 GGCCAAATTTGCGCAATCCCAACCTCCATCATCTGACCAACCTCCTGCTCCCACTGCT 696
DB 302 GGCCAAATTTGCGCAATCCCAACCTCCATCATCTGACCAACCTCCTGCTCCCACTGCT 361
QY 697 CCGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
DB 362 CCGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
QY 757 TGCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 816
DB 422 TGCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 817 ATTCAGAGATCTTCAACCAACGAGACCAATGCAAGCTGACAGACTCTGCTCA 876
DB 482 ATTCAGAGATCAACCAACGAGACCAATGCAAGCTGACAGACTCTGCTCA 541
QY 877 GGAACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 936
DB 542 GGAACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
QY 937 ATTCATCCATCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 996
DB 602 ATTCATCCATCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
QY 997 TTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056
DB 662 TTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
QY 1057 GTTGGCTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1116
DB 722 GTTGGCTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 781
QY 1117 AGTCCCTTTTACCGCTGTTACCAATTTCTTTGCTTTTGGGTATACATTTAAACCTTA 1176
DB 782 AGTCCCTTTTACCGCTGTTACCAATTTCTTTGCTTTTGGGTATACATTTAAACCTTA 841
QY 1177 ATAA 1181
DB 842 ACAA 846
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RESULT 13

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US-10-209-264-1
; Sequence 1, Application US/10209264
; Publication No. US20030003111A1
; GENERAL INFORMATION:
; APPLICANT: Oon, Chong Jin
```

```

1 / Lim, Gek Keow
2 / Zhao, Yi
3 / Chen, Wei Ning
4 / TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
5 / USES THEREOF
6 /
7 / NUMBER OF SEQUENCES: 11
8 / CORRESPONDENCE ADDRESS:
9 / ADDRESSEE: Ladas & Parry
10 / STREET: 26 West 61 Street
11 / City: New York
12 / STATE: New York
13 / COUNTRY: USA
14 / ZIP: 10023
15 /
16 / COMPUTER READABLE FORM:
17 / MEDIUM TYPE: floppy disk
18 / COMPUTER: IBM PC compatible
19 / OPERATING SYSTEM: PC-DOS/MS-DOS
20 / SOFTWARE: Patent In Release #1.0, Version #1.30
21 / CURRENT APPLICATION DATA:
22 / APPLICATION NUMBER: US/10/209,264
23 / FILING DATE: 31-Jul-2002
24 / CLASSIFICATION: 435
25 / PRIOR APPLICATION DATA:
26 / APPLICATION NUMBER: PCT/SG98/00046
27 / FILING DATE: 19-JAN-1998
28 / ATTORNEY/AGENT INFORMATION:
29 / NAME: Maas, Clifford J.
30 / REGISTRATION NUMBER: 30,086
31 / REFERENCE/DOCKET NUMBER: U-013109-7
32 / TELECOMMUNICATION INFORMATION:
33 / TELEPHONE: (212) 708-1800
34 /
35 / INFORMATION FOR SEQ ID NO: 1:
36 /
37 / SEQUENCE CHARACTERISTICS:
38 / LENGTH: 3215 base pairs
39 / TYPE: nucleic acid
40 / STRANDEDNESS: double
41 / TOPOLOGY: circular
42 /
43 / SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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45 / US-10-209-264-1
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Db      420  TATGCGCATCTTCTTGTTGGTTCCTTGAGACTACCAAGTATGTTGCCCTTGTCTTC      479
QY      815  TAAATTCAGAGATCTTCAACCAACAGACGGGACCATGACAGACCTGCACGACTCCTGCTC      874
Db      480  TACTTCCAGGAACATCAACCAACAGACGGGGCCATGCAAGACTGCACGACTCCTGCTC      539
QY      875  AAGGAACTCTATGATATCCCTTCCTGTTGCTGTGACAAAACCTTCGGATGGAAATGACCT      934
Db      540  AAGGAAATCTACGTTTCCCTTCCTGTTGCTGTGACAAAACCTTCGGACGGAAATGACCTT      599
QY      935  GTATTCCCATCCCATCATCTCTGAGGCTTTCGGAAATTCCTATGGAGAGTGGGCTCAGCC      994
Db      600  GTATTCCCATCCCATCATCTCTGAGGCTTTCGGAAATTCCTATGGAGAGTGGGCTCAGTCC      659
QY      995  GTTTCCTCGCTCAGTTTACTAGTGCACATTTGTTCACTGATGTTGAGGCTTTTCCCCA      1054
Db      660  GTTTCCTCGCTCAGTTTACTAGTGCACATTTGTTCACTGATGTTGAGGCTTTTCCCCA      719
QY      1055  CTGTTTGGCTTTCAGTTATATGAGATGATGTGTACTGGGGGCCAAGTCTGTACACATCT      1114
Db      720  CTGTTTGGCTTTCAGTTATATGAGATGATGTGTATTTGGGGGGAAGTCTGTACAAATCT      779
QY      1115  TGAGTCCCTTTTACCGCTGTACCAATTTTCTTGTCTTGGGATATACATTTAAACC      1174
Db      780  TGAGTCCCTTTTACCTCTATATACCAATTTTCTTGTCTTGGGATATACATTTAAACC      839
QY      1175  TAAATAA  1181
Db      840  TAAATAA  846

RESULT 14
US-10-142-358-1
; Sequence 1, Application US/10142358
; Publication No. US20030083291A1
GENERAL INFORMATION:
APPLICANT: Michel, Marie-Louise
Mancine, Maryline
TITLE OF INVENTION: Nucleotide Vector, Composition
Containing Such Vector, and Vaccine for Immunization
Against Hepatitis
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
Dumer
ADDRESSSEE: Finegan, Henderson, Farabow, Garrett &
Dumer
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/142,358
FILING DATE: 10-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/799,569
FILING DATE: 12-FEB-1997
APPLICATION NUMBER: US 08/706,337
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 08/633,821
FILING DATE: 22-APR-1996
APPLICATION NUMBER: FR 94/00483
FILING DATE: 27-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0128-01000

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-142-358-1

Query Match 58.7%; Score 693; DB 14; Length 5618;
Best Local Similarity 96.6%; Pred. No. 1.9e-214;
Matches 708; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

449 TATGCTCATCTTCTCGAGGATTTGGGACCTCGCGGAACTGGAGAAATCATCATCAG 508
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898 TACCGGGCCCCCTCGAGGATTTGGGACCTCGCGTGAACATGAGAAATCATCATCAG 957
509 GATTCCTAGGACCCCTCGCTCGTTACAGGGGGGTTTCTGTTGACAAAGATCCCA 568
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958 GATTCCTAGGACCCCTCGCTCGTTACAGGGGGGTTTCTGTTGACAAAGATCCCA 1017
569 CAATACCGGAGAGTCTAGACTCGTGAGTCTCTCAATTTCTAGGGGAACTACCG 628
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1198 TGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1257
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1258 GTCTCTAATTCAGAGATCTTCAACCAACGAGACGAGACATGACAGCTGACAGCTC 1317
869 CTGCTCAAGGAACCTCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
1318 CTGCTCAAGGAACCTCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
929 GCACCTGATTCAGATCCATCATCTGAGGCTTTGGGAAATTCCTATGGAGTGGGCT 988
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1049 CCCCCACTGTTGGCTTCACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1108
1498 CCCCCACTGTTGGCTTCACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1557
1109 CCATCTGAGTCCCTTTTACCGCTTACCAATTTCTGTTGCTGTTGGGATACATTT 1168
1558 GCATCTTGAATCCCTTTTACCGCTTACCAATTTCTGTTGCTGTTGGGATACATTT 1617
1169 AAACCTATATAA 1181
1618 AAACCTAACA 1630

RESULT 15
US-09-821-877-6
; Sequence 6, Application US/09821877

Patent No. US20020177124A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Coleman, Paul F.
APPLICANT: Mushahwar, Isha K.
TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
TITLE OF INVENTION: And Methods Of Detection Thereof
FILE REFERENCE: 6794.US.01
CURRENT APPLICATION NUMBER: US/09/821,877
CURRENT FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 690
TYPE: DNA
ORGANISM: Hepatitis B Virus
OTHER INFORMATION: Mutant Hepatitis B Virus Strain
US-09-821-877-6

Query Match 58.4%; Score 690; DB 10; Length 690;
Best Local Similarity 100.0%; Pred. No. 5.9e-214; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

481 GCGCGGAACATGAGAACATCATCAGATTCCTAGGACCCCTGCTGTTACAGCG 540
1 GCGCGGAACATGAGAACATCATCAGATTCCTAGGACCCCTGCTGTTACAGCG 60
541 GGGTTTCTTGTGACAAAGATCTCTCAATACCGGAGATCTAGACTCGTGTGAGCT 600
61 GGGTTTCTTGTGACAAAGATCTCTCAATACCGGAGATCTAGACTCGTGTGAGCT 120
601 TCTCTCAATTTCTAGGGGGAACTACCGTGTGCTGAGCAAAATTCGAGTCCCAACC 660
121 TCTCTCAATTTCTAGGGGGAACTACCGTGTGCTGAGCAAAATTCGAGTCCCAACC 180
661 TCCATCACTACCAACCTCTGCTCTCAACTTGTCTGTTATGCTGATGCTGCTG 720
181 TCCATCACTACCAACCTCTGCTCTCAACTTGTCTGTTATGCTGATGCTGCTG 240
721 CCGGCTTTATCATCTTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
241 CCGGCTTTATCATCTTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
781 CTGACCTATCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
301 CTGACCTATCAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
841 ACGGACCATGACAGCTGACAGCTCTGCTCAAGGAACCTCTATGATTCCTCTGT 900
361 ACGGACCATGACAGCTGACAGCTCTGCTCAAGGAACCTCTATGATTCCTCTGT 420
901 TGTGTTACAAAACCTTGGATGAGAACTGACCTGATATTCATCCATCATCTGAGCT 960
421 TGTGTTACAAAACCTTGGATGAGAACTGACCTGATATTCATCCATCATCTGAGCT 480
961 TTGGAAAAATTCATGAGGATGAGGCTCAACCGCTTCTCTGCTGATGTTACTAGTG 1020
481 TTGGAAAAATTCATGAGGATGAGGCTCAACCGCTTCTCTGCTGATGTTACTAGTG 540
1021 CCATTTGTCAGTGTGCTGAGGCTTCCCACTGTTTGGCTTCACTATATGATG 1080
541 CCATTTGTCAGTGTGCTGAGGCTTCCCACTGTTTGGCTTCACTATATGATG 600
1081 ATGTTGATCGGGGCCAAGTCTGACACATCTTGAAGTCCCTTTTACCGCTGTACCA 1140
601 ATGTTGATCGGGGCCAAGTCTGACACATCTTGAAGTCCCTTTTACCGCTGTACCA 660
1141 ATTTCTTTTGTCTTGGGTATACATTTAA 1170
661 ATTTCTTTTGTCTTGGGTATACATTTAA 690

Tue Sep 16 09:06:12 2003

us-09-821-877-1.rmpb

Page 12

Search completed: September 15, 2003, 03:56:35
Job time : 263 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2003, 01:23:11; Search time 1985 Seconds
(without alignments)
14460.245 Million cell updates/sec

Title: US-09-821-877-1

Perfect score: 1181
Sequence: 1 atggggcagaatcttccac.....tacatttaaccctaataa 1181

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	45.8	3.9	997	29	CNS005TE	AL060767 Drosophila
2	45.6	3.9	636	28	AZ038456	AZ038456 RPT-23-2
3	45.6	3.9	885	13	BX425603	BX425603 BX425603
4	43.2	3.7	779	29	BZ696852	BZ696852 SP_Ba008

C 5	42.6	3.6	602	28	AZ372526	AZ372526 1M0124L21
6	42.4	3.6	1201	13	BX381961	BX381961
7	41.8	3.5	1101	29	CNS016LW	AL106910 Drosophila
8	41.6	3.5	308	28	AZ879026	AZ879026 RPT-23-1
9	41.1	3.5	377	28	AZ413108	AZ413108 1M0197017
C 10	41.1	3.5	745	28	BH034701	BH034701 RPT-24-2
C 11	40.8	3.5	697	28	BH063007	BH063007 RPT-24-3
12	40.6	3.4	629	9	AV647972	AV647972 AV647972
13	40.3	3.4	512	28	AZ938251	AZ938251 2M0196F16
14	40.3	3.4	520	28	BZ128636	BZ128636 CH230-440
C 15	40.3	3.4	1101	29	CNS016B8	AL106526 Drosophila
C 16	39.8	3.4	1254	29	AG072222	AG072222 Pan trogl
C 17	39.6	3.4	450	28	AZ097652	AZ097652 RPT-23-1
C 18	39.4	3.3	548	28	BH107673	BH107673 RPT-23-3
C 19	39.4	3.3	644	10	BB641359	BB641359 BB641359
C 20	39.4	3.3	681	29	CNS02FE9	AL194922 Tetradon
C 21	39.4	3.3	1003	29	CNS01TT3	AL166844 Tetradon
22	39.4	3.3	1201	13	BX337072	BX337072 BX337072
23	39.4	3.3	1653	11	AK043679	AK043679 Mus muscu
24	39.2	3.3	292	28	AZ637334	AZ637334 1M0496108
C 25	39.2	3.3	987	29	CNS00418	AL066537 Drosophila
C 26	39.2	3.3	1101	29	CNS0181N	AL108773 Drosophila
C 27	39.2	3.3	1201	13	BX376097	BX376097 BX376097
C 28	39.2	3.3	239	10	BF778098	BF778098 NX51-077
C 29	39.2	3.3	555	28	AZ882512	AZ882512 RPT-23-2
C 30	39.2	3.3	621	12	BM492837	BM492837 NXRV-031
C 31	39.2	3.3	705	12	BM902701	BM902701 NX1V-057
C 32	39.2	3.3	972	29	CNS02BJT	AL189928 Tetradon
C 33	39.2	3.3	985	9	AL575191	AL575191 AL575191
C 34	39.2	3.3	1036	12	BM011009	BM011009 603634682
C 35	39.2	3.3	1212	29	BZ560978	BZ560978 pac82-164
36	38.8	3.3	885	13	BX425603	BX425603 BX425603
37	38.6	3.3	597	28	AZ067459	AZ067459 RPT-23-4
C 38	38.6	3.3	611	14	CB580512	CB580512 AMGNUT-C
C 39	38.4	3.3	668	28	AZ312109	AZ312109 1M0027K13
C 40	38.4	3.3	824	10	BF241268	BF241268 60187873
C 41	38.4	3.3	974	13	BX344914	BX344914 BX344914
42	38.4	3.3	1101	29	CNS00330	AL063790 Drosophila
43	38.2	3.2	214	9	AI053945	AI053945 q171h02.x
C 44	38.2	3.2	463	12	BT160947	BT160947 602865330
45	38.2	3.2	492	28	BZ180127	BZ180127 CH230-349

ALIGNMENTS

RESULT 1
CNS005TE 997 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR12K22 of RPT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL060767.1 GI:4943573
VERSION AL060767
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mammos in Pieter de Jong's laboratory in the Department of

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL COMMENT

Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0124 row: L column: 21
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 602.

FEATURES

source

1. .602
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0124L21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gii4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

320 a 48 c 197 g 37 t

ORIGIN

Query Match 3.6%; Score 42.6; DB 28; Length 602;
Best Local Similarity 49.3%; Pred. No. 4.9;
Matches 111; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY TCTCAATTTTCAGGGGAACACGCTGCTGGCCAAATTCGAGTCCCAACCTC 662
Db TCTCTCTGTTC 167
QY 663 CAATCATCAACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 722
Db 166 TCT 107
QY 723 GCGTTATATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 106 TCTTCT 47
QY 783 GACATATCAAGATGTCGCCGTTGTCCTTAATTCAGATC 827
Db 46 CT 2

RESULT 6

EX381961 1201 bp mRNA linear EST 08-MAY-2003
LOCUS EX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1072YF05 3-PRIME, mRNA sequence.

ACCSSION VERSION KEYWORDS SOURCE ORGANISM

EX381961.1 GI:30453007
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1. (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished

JOURNAL COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1072C03NP1.

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YF05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT

95 a 191 c 115 g 55 t 745 others

ORIGIN

Query Match 3.6%; Score 42.4; DB 13; Length 1201;
Best Local Similarity 2.6%; Pred. No. 7.4;
Matches 10; Conservative 111; Mismatches 264; Indels 0; Gaps 0;

QY 768 CTGTGGTCTCTCTGAGTATCAAGTATGTTGCCGTTGCTCTTAATTCAGATC 827
Db 410 MNKKKKKKCMKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKNN 469
QY 828 TTCAACCAAGACAGACGACATGACAGAGCTCCCTGCTCAAGAACTCTAT 887
Db 470 KNNNNNNNNKNN 529
QY 888 GTATCCCTCCTGTGCTGTACAAACCTTCGATGGAACCTGATATTCATCC 947
Db 530 NCKKNN 589
QY 948 ATCATCCTGGGCTTTTGGAAAATTCCTATGGAAGTGAGCCCTAGCCGTTTCTCTGGCT 1007
Db 590 NKNNN 649
QY 1008 CAGTTTACTAGTGCATTTGTCAGTGCTTCGTAAGGCTTTCCCACTGTTGGCTTC 1067
Db 650 NNN 709
QY 1068 AGTTATATGATATGTTGACTGGGGGCAAGTGTGACACATCTGATGCTCTTTT 1127
Db 710 KKTNNKKKNNKNN 769
QY 1128 ACCGCTGTACCAATTTCTTTTGT 1152
Db 770 NNN 794

RESULT 7
CNS016LM

FEATURES	Location/Qualifiers
source	1. .1101

Query Match	3.5%	Score	41.8	DB	29	Length	1101
Best Local Similarity	10.4%	Pred. No.	10				
Matches	35	Conservative	91	Mismatches	211	Indels	0
						Gaps	0

[illegible]

RESULT	8
AZ879026	
LOCUS	AZ879026
DEFINITION	RPCR-23-193P13.TU RPCR-23 Mus musculus genomic clone RPCR-23-193P13
ACCESSION	AZ879026

REFERENCE AUTHORS

COMMENT

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: szhaow@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderinfo.htm>). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 193 row: P column: 13
Seq primer: SP6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .308

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-193P13"
/sex="Female"
/lab_host="DH10B"
/clone_1id="RPCI-23"
/notes="Organ: Kidney/Brain; Vector: pBac3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Site
selected DNA was cloned into the pBac3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

```

BASE COUNT	28 a	130 c	35 g	115 t
ORIGIN				

Query Match	3.5%	Score 41.6	DB 28	Length 308
Best Local Similarity	49.5%	Pred. NC 6.8		
Matches 107, Conservative	0	Mismatches 109	Indels 0	Gaps 0

[illegible]

RESULT 9			
AZ43108			
LOCUS	377 bp	DNA	linear
DEFINITION	AZ43108		
	IM019701F Mouse 10kb plasmid UUC1M library Mus musculus genomic		

ACCESSION	clone UGIC1M0197017 F, genomic survey sequence.
VERSION	AZ413108
KEYWORDS	AZ413108.1 GI:10537121
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 377)
TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Neenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT	plasmid inserts unpublished Contact: Robert B. Weiss

FEATURES	Location/Qualifiers
source	1. .377

BASE COUNT
ORIGIN

44 a 136 c 25 g 172 t

/'organism="Mus musculus"
/'mol_type="genomic DNA"
/'strain="C57BL/6J"
/'db_xref="taxon:10090"
/'clone="UUCGCM0197017"
/'sex="Male"
/'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/'clone_1ib="Mouse 10kb Plasmid UUCGCM library"
/'note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	3.5%	Score 41	DB 28	Length 377
Beet Local Similarity	56.2%	Pred. No. 11		
Matches	77	Conservative	0	Mismatches 60; Indels 0; Gaps 0;
QY	645	TTGCGAGTCCCACTCCATCACTCAACCACTGCTCTCCAACTGTCGGGTGA	704	
Db	204	TTCTCTTTCTCTTC	263	
QY	705	TGCGTAGATGTCTGCGGCGTTTTATATCATCTTCCCTTCATCGTACGTATGCGCAT	764	
Db	264	TTCTCTTTCTTTCTTTCTTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTT	323	

Oy 765 CTCTGTGTGTTCTTC 781
 ||||| |||||
 Db 324 CTCTCTCTCTTCTTC 340
 ||||| |||||

RESULT	10
BH034701/c	
LOCUS	
DEFINITION	
ACCESSION	BH034701
VERSION	RPCI-24-267K17.TU RPCI-24 Mus musculus genomic clone RPCI-24-267K17 genomic survey sequence.
KEYWORDS	BH034701
SOURCE	BH034701.1 GI:14807809
ORGANISM	GSS
Mus musculus	(house mouse)

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus					
Eukaryota Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:					
Mammalia: Eutheria: Rodentia: Scurionath: Muridae: Murinae: Mus.					
1 (bases 1 to 745)					
Zhao, S., Niemman, W., Malek, J., Shatman, S., Akincet, B., Levins, M.,					
Tsagay, G., Geet, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,					
Russell, D., de Jong, P. and Fraser, C.M.					
Mouse BAC End Sequences from Library RPCI-24					
Unpublished					
Other GSSs: RPCI-24-267K17.TV					

Contact: Shanying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPECI-24. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choiri.org/bacpac/orderingframe.html>). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 267 row: K column: 17
Seq primer: SP6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. 745
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	/mol_type="genomic DNA"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="RPC1-24-267K17"
	/sex="Male"
	/cell_type="Spleen/Brain"
	/clone_id="RPC1-24"
	/note="Vector: pTRABAC1; Site 1: BamH1; Site 2: BamH1; The RPC1-24 Mouse BAC library produced by Peter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT	347 a 70 c 239 g 89 t
ORIGIN	
Query Match	3.5%; Score 41; DB 28; Length 745;
Best Local Similarity	53.4%; Pred. No. 14;
Matches 86; Conservative	0; Mismatches 75; Indels 0; Gaps 0;

QY CCGCAATACACCAACCTCTGACGCGCAAACTGATGCTGATAGCGTAGATGCT 719
Db CTTCT 544
QY GGGGGGTTTATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 779
Db CTTCT 484
QY TCTGACATCAAGGTATGCGCGTATGCTCTTAATTC 820
Db TCTTCT 443

RESULT	11
BH063007/c	
LOCUS	BH063007.c
DEFINITION	BH063007 697 bp DNA linear GSS 18-JUL-2001 RPCT-24-35SL19.TU RPCT-24 Mus musculus genomic clone RPCT-24-35SL19
ACCESSION	BH063007
VERSION	BH063007.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 697) Zhao,S., Niemann,W., Malek,J., Shatman,S., Akintc,B., Levins,M., Tessaghe,G., Geer,K., Kroll,M., Shvartsbeyn,A., Gebregorgis,E., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCT-24 Unpublished
TITLE	Other_GSSs: RPCT-24-35SL19.TV
JOURNAL	
COMMENT	

FEATURES	Location/Qualifiers
source	1. .697

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPC1-24-355L1.9"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_11b="RPC1-24"
/notes="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPC1-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

```

BASE COUNT	353 a	38 c	251 g	55 t	
Query Match	3.5%;	Score 40.8;	DB 28;	Length 697;	
Best Local Similarity	48.7%;	Pred. No. 15;			
Matches 11;	Conservative 0;	Mismatches 117;	Indels 0;	Gaps 0	
Qy	603	TCTCATATTTCTAGGGGAACTACCGTGTCGTGTGGCCAAATAATCGAGTCCCAACTC	662		
Db	598	TCTGTGTTCTTCTGTCTGTGCTCTGCTACCTTCTTCTTCTTCTTCTTCTTCTC	539		
Qy	663	CAATCACTACCAACTCTCTGTCCTCAACTGTCCTGATACGATGTCGCG	722		
Db	538	TTCCTCTGTCCT	479		
Qy	723	GCGTTTATCATTTTCTCTTCACTGCTGCTAAGCTCAATCTTGTGTGTTCTT	782		
Db	478	CTTCT	419		
Qy	783	GGACTATCAAGGATGTGCGCGTTGTCCTCAATACAGAGATCTTC	830		
Db	418	TGCGTTTGACTTTTCTCTCTTTCATATCTCTTCTCTCTCTCTCTCTCTCTCT	371		

RESULT	12
AV647972	
LOCUS	629 bp mRNA linear EST 15-JAN-2002
DEFINITION	AV647972 GLC Homo sapiens cDNA clone GICBHD10_3', mRNA sequence.
ACCESSION	AV647972
VERSION	AV647972.1 GI:9868986
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (pages 1 to 629)
AUTHORS
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,

TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE	21625106
PUBMED	11752456
COMMENT	Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel.: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

```
FEATURES      Location/Qualifiers
source        1. .629
```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICBDH10"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_id="GIC"
/notice="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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Query Match	3.4%	Score 40.6	DB 9	Length 629
Best Local Similarity	52.7%	Pred. No. 17		
Matches	88	Conservative	0	Mismatches 79
				Indels 0
				Gaps 0
Oy	1014	ACTAGTCCATTGTTGTCAGTGTGCGAGGAGCTTCCCCAGCTGTGGCTTTCAGTTAT	1073	
Db	10	ACTAGTACGAGGAGTACAGGCTTATACATCTTTGCTATTATCAGACTATATTTCAT	69	
Oy	1074	ATGAGTATGTTGTTACTGGGGGCCAAGCTCTGTACACCATCTTGAGTCCCTTTTACCGCT	1133	
Db	70	CTTATATATATCTGATTTGCTGCACAAATGTAGAGCTGCAAGTGCAGAGCCTTTCAATGCT	129	
Oy	1134	GTTACCAATTTCTTTTGTCTTTGGGATATCATTTAAACCTATAAA	1180	
Db	130	ACCTCCAACTGCTTAACCGTATAGGATATAGATACAACTTACTCA	176	

RESULT	13
LOCUS	AZ938251
DEFINITION	AZ938251 512 bp DNA linear GSS 26-Apr-2001
ACCESSION	U00196F16R Mouse 10kb plasmid U00C2M library Mus musculus genomic
VERSION	clone U00C2M0196F16 R, genomic survey sequence.
KEYWORDS	AZ938251
SOURCE	AZ938251.1 GI:13797782
ORGANISM	GSS.
	Mus musculus (house mouse)
	Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 512)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mamoud, M., Meenen, E., Petersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0196 row: F column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 512.
Location/Qualifiers

FEATURES

source

1. 512
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0196F16"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PWD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

91 a 172 c 56 g 193 t

Query Match

Best Local Similarity 3.4%; Score 40; DB 28; Length 512;
Matches 91; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db

645 TTGCGAGTCCCAACTTCACATCACTCAACCTCTGTCCTCAACTGTCGTTA 704
|||||
302 TTCT 361
|||||

Qy

705 TCGGTGATGTCGTGGGGGTTTATCATCTCTCTCACTGTCGTCATGCCCAT 764
|||||

Db

362 TCT 421
|||||

Qy

765 CTCTCTGTCGTCCTCTGACATCAAGTATGTCGTCCTTAATTC 820
|||||

Db

422 TCT 477
|||||

RESULT 14

B2128636

LOCUS

B2128636 520 bp DNA linear GSS 11-OCT-2002
CH230-440G9.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-440G9. genomic survey sequence.

DEFINITION

B2128636
B2128636.1 GI:23769583

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 520)

REFERENCE

AUTHORS

Zhao, S., Shetty, J., Shateman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 Mbol segment
Unpublished
Other GSSs: CH230-440G9.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

JOURNAL

COMMENT

Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or_exting_information.htm). BAC end page: http://www.tigr.org/tcdb/bac_ends/rat/bac_end_intro.html
Plate: 440 row: G column: 9
Seq primer: T7
Class: BAC ends.
Location/Qualifiers

FEATURES

source

1. 520
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-440G9"
/sex="Female"
/cell_type="Brain"
/clone_1b="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"

BASE COUNT

22 a 257 c 8 g 233 t

Query Match

Best Local Similarity 3.4%; Score 40; DB 28; Length 520;
Matches 88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Db

652 TCCCAACTTCATATCACTCAACACTCTGTCCTCAACTGTCGTTATGCTGG 711
|||||

Qy

311 TCT 370
|||||

Db

371 CTTCCCT 430
|||||

Qy

712 ATGTGTCGGGGGTTTATCATCTCTCTTCAATCTGCTGTCATGCTATCTTGG 771
|||||

Db

772 TTGGTCTTGTGACATCAAGTATGTCGTCCTTAATTC 819
|||||

Qy

431 CTCTCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478
|||||

RESULT 15

CNS016B8 1101 bp DNA linear GSS 26-JUL-1999
LOCUS
DEFINITION
CNS016B8
Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN15B23 of DrosBAC library from Drosophila melanogaster (fruit

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